

From: Snedden, Sheridan
Sent: Monday, February 03, 2003 7:29 PM
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Subject: Sequence Search 09701463

Sheridan SNEDDEN ID# 79298 Date: 2/3 /2002

AU 1653

308-4843

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1). Search for SEQ ID NO: 1

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Thanks,
Examiner Snedden
#79298
A.U. 1653/ 9B01
Office Location: 10A12
Phone #: 305-4843

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

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NA Sequences: _____
AA Sequences: / _____
Structures: _____
Bibliographic: _____
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Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

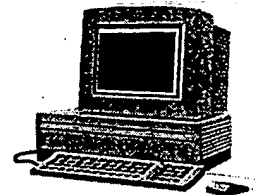
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Search Results

Feedback Form (Optional)



Scientific & Technical Information C

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search *or contact*:

Mary Hale, Supervisor, 308-4:
CM-1 Room 1E01

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* (Example: 1610)

➤ *Relevant prior art found, search results used as follows:*

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Search results were not useful in determining patentability or understanding the invention.

Other Comments:

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or mary.hale@uspto.gov

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OM protein - protein search, using sw model

Run on: February 4, 2003, 10:02:20 ; Search time 37 Seconds
(without alignments)
993.978 Million cell updates/sec

Title: US-09-701-463-1
Perfect score: 1504
Sequence: 1 OENODGRYSITYTGLSKH.....SCHVSHSLAQLPVPWEAS 276

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_101002:.*
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2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SID2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SID2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SID2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1504	100.0	276	21	AA49442
2	910	60.5	170	21	AA43662
3	800.5	53.2	163	21	AA80275
4	791	52.6	171	20	AA70773
5	525	34.9	274	9	AA80911
6	511	34.0	365	21	AA68268
7	511	34.0	365	21	AA52922
8	511	34.0	365	22	AA58683
9	510	33.9	93	22	AB83939
10	510	33.9	93	22	AB82481

11	510	33.9	93	22	AA60079	Human brain expres
12	510	33.9	93	22	AA72688	Human bone marrow
13	510	33.9	93	22	AA32919	Peptide #6956 enco
14	510	33.9	93	23	AB842512	Human peptide enco
15	509	33.8	369	22	AA02882	Novel human secret
16	507	33.7	365	21	AA58266	Human leukocyte an
17	507	33.7	365	21	AA58290	Human leukocyte an
18	507	33.7	365	21	AA52920	HLA-A2/A28 family
19	507	33.7	365	21	AA52924	HLA-A2/A28 family
20	507	33.7	365	22	AA58681	HLA-A2/A28 protein
21	507	33.7	365	22	AA58685	HLA-A2/A28 protein
22	505	33.6	365	21	AA58269	Human leukocyte an
23	505	33.6	365	21	AA52923	HLA-A2/A28 family
24	504	33.5	365	22	AA58684	Human leukocyte an
25	504	33.5	365	21	AA58272	Human leukocyte an
26	504	33.5	365	21	AA52926	HLA-A2/A28 family
27	504	33.5	365	22	AA58687	HLA-A2/A28 protein
28	503	33.4	274	21	AA58276	Human leukocyte an
29	503	33.4	274	21	AA52930	HLA-A2/A28 family
30	503	33.4	274	22	AA58691	HLA-A2/A28 protein
31	503	33.4	362	8	AA70155	Sequence encoded b
32	503	33.4	365	21	AA58265	Human leukocyte an
33	503	33.4	365	21	AA58271	Human leukocyte an
34	503	33.4	365	21	AA52919	HLA-A2/A28 family
35	503	33.4	365	21	AA52925	HLA-A2/A28 family
36	503	33.4	365	22	AA58680	HLA-A2/A28 protein
37	503	33.4	365	22	AA58686	HLA-A2/A28 protein
38	502.5	33.4	337	8	AA70590	Sequence of the hu
39	502	33.4	366	20	AA70733	Breast cancer asso
40	500	33.2	274	21	AA58275	Human leukocyte an
41	500	33.2	274	21	AA52929	HLA-A2/A28 family
42	500	33.2	274	22	AA58690	HLA-A2/A28 protein
43	497	33.0	274	21	AA58274	Human leukocyte an
44	497	33.0	274	21	AA52928	HLA-A2/A28 family
45	497	33.0	274	22	AA58689	HLA-A2/A28 protein

ALIGNMENTS

RESULT 1	
AA49442	AA49442 standard; protein; 276 AA.
XX	
AC	AA49442;
XX	
DT	17-MAR-2000 (first entry)
XX	
DE	Human plasma Zn-alpha2-glycoprotein.
XX	
KW	Lipid mobilizing agent; zinc alpha2-glycoprotein; adenylate cyclase;
KW	fat metabolism; muscle synthesis; obesity; type II diabetes; body weight;
KW	muscle development; cachexia-inducing tumor; lipolysis; antitumor; cancer; human.
KW	
OS	Homo sapiens.
XX	
PN	W09962939-A2.
XX	
PD	09-DEC-1999.
XX	
PF	01-JUN-1999; 99WO-GB01509.
XX	
PR	29-MAY-1998; 98GB-0011465.
XX	
PA	(TISD/) TISDALE M J.
PA	(TODO/) TODOROV P T.
XX	
PI	Tisdale MJ, Todorov PT;
XX	
DR	WPI; 2000-072831/06.
XX	
PT	New lipid mobilizing agent used for treating obesity, and as diagnostic

PT marker for cancer
 XX
 PS Claim 3; Fig 1; 63pp; English.
 XX
 CC The invention provides a therapeutic lipid mobilizing agent (I) that has
 CC the properties and characteristics of a zinc alpha2-glycoprotein, or its
 CC fragments, and had apparent relative molecular weight (Mr) determined by
 CC gel exclusion chromatography) over 6 kD. (I) stimulates adenylate cyclase
 CC activity in a guanosine diphosphate-dependent process (in murine
 CC adipocyte plasma membranes). In vivo it increases metabolism of fat and
 CC may stimulate protein (muscle) synthesis. (I) is used: to treat obesity;
 CC (particularly in subjects at high risk of developing type II diabetes) or
 CC to reduce body weight; to stimulate muscle development; as diagnostic
 CC marker for cachexia-inducing tumors; to identify or investigate agents
 CC that inhibit lipolysis (potential anticachectic or antitumor agents) and
 CC to raise specific antibodies (Ab). The Ab are used: for diagnostic
 CC detection of (I); as inhibitor or antagonist for treatment of cachexia-
 CC inducing cancers and/or tumors, and for affinity purification of (I);
 CC (I) induces a loss in body weight by specific deletion of fat; i.e. It
 CC does not reduce muscle mass. The present sequence represents the complete
 CC amino acid sequence of the human plasma Zn-alpha2-glycoprotein, as
 CC published by T. Araki et al. (1988).
 XX
 SO Sequence 276 AA:
 Query Match 100.0%; Score 1504; DB 21; Length 276;
 Best Local Similarity 100.0%; Pred. No. 2.6e-123;
 Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QENOGGRSLTYITTYGLSKHVEDVPAFOALGSLNDLQFRYNSKDKRSQPMGLMROVEGM 60
 Db 1 QENOGGRSLTYITTYGLSKHVEDVPAFOALGSLNDLQFRYNSKDKRSQPMGLMROVEGM 60
 QY 61 EDWKEDSOLQKAREDMETLKDIEVEYNDNSGSHVLQGRFCIEIENRRSSGAFWKYYDGGK 120
 Db 61 EDWKEDSOLQKAREDMETLKDIEVEYNDNSGSHVLQGRFCIEIENRRSSGAFWKYYDGGK 120
 QY 121 DYIEFNKEIPAVPPDPAQITKQKWEAEFVYQRAKAYLEECPCATLTKRYTKYSNIID 180
 Db 121 DYIEFNKEIPAVPPDPAQITKQKWEAEFVYQRAKAYLEECPCATLTKRYTKYSNIID 180
 QY 181 RODPSVAVTSHQAPGEKKKLCIAVDYFPGKIDVHMTAGOVQEPBELGDVLIHNGNGTY 240
 Db 181 RODPSVAVTSHQAPGEKKKLCIAVDYFPGKIDVHMTAGOVQEPBELGDVLIHNGNGTY 240
 QY 241 QSMVVAVPPODTAPYSCHVQSSLAQPLVWPWEAS 276
 Db 241 QSMVVAVPPODTAPYSCHVQSSLAQPLVWPWEAS 276
 RESULT 2
 AAB43862
 ID AAB43862 standard; Protein; 170 AA.
 XX
 AC AAB43862;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human cancer associated protein sequence SEQ ID NO:1307.
 XX
 KM Human; cancer associated gene; cancer antigen; detection; cancer;
 KM diagnosis; cytostatic; proliferative; vulnerable; immunomodulator;
 KM antidiabetic; antiasthmatic; antirheumatic; antithyroid; antiviral;
 KM antiinflammatory; antihypertensive; antiallergic; antibacterial; cardiant;
 KM dermatological; neuroprotective; thrombolytic; coagulant; neotropic;
 KM vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
 KM immune disorder; haematopoietic cell disorder; autoimmune disorder;
 KM allergic reaction; graft versus host disease; organ rejection;
 KM haemostatic; thrombolytic; cardiovascular disorder; infection;
 KM neurological disease; drug screening.
 XX
 OS Homo sapiens.
 XX

PN WO20005350-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US05882.
 XX
 PR 12-MAR-1999; 99US-0124270.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI: 2000-587533/55.
 DR N-PSDB; AAC78071.
 XX
 PT Novel isolated nucleic acids comprising sequences encoding peptides
 PS useful for treating or diagnosing e.g. cancer -
 XX
 PS Claim 11; Page 1954; 2352pp; English.
 XX
 CC AAC77607 to AAC78448 encode the human cancer associated proteins given
 CC in AAB43398 to AAB44239. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC include: cytostatic; proliferative; vulnerable; immunomodulator;
 CC antidiabetic; antiasthmatic; antirheumatic; antithyroid;
 CC antiinflammatory; antihypertensive; antiallergic; antibacterial; antiviral;
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
 CC neotropic; vasotropic; antipsoriatic and antiangiogenic. The
 CC polynucleotides and polypeptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological diseases and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of
 CC the present invention.
 XX
 SO Sequence 170 AA:
 Query Match 60.5%; Score 910; DB 21; Length 170;
 Best Local Similarity 99.4%; Pred. No. 1.1e-71;
 Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 112 FWKYYVDGKDYIEFNKEIPAVPPDPAQITKQKWEAEFVYQRAKAYLEECPCATLTKRY 171
 Db 6 FWKYYVDGKDYIEFNKEIPAVPPDPAQITKQKWEAEFVYQRAKAYLEECPCATLTKRY 65
 QY 172 LKYSKNIIDRODPPSVVYTSHQAPGEKKKLCIAVDYFPGKIDVHMTAGOVQEPBELRGD 231
 Db 66 LKYSKNIIDRODPPSVVYTSHQAPGEKKKLCIAVDYFPGKIDVHMTAGOVQEPBELRGD 125
 QY 232 VLIHNGNGTYQSMVVAVPPODTAPYSCHVQSSLAQPLVWPWEAS 276
 Db 126 VLIHNGNGTYQSMVVAVPPODTAPYSCHVQSSLAQPLVWPWEAS 170
 RESULT 3
 AAB80275
 ID AAB80275 standard; Protein; 183 AA.
 XX
 AC AAB80275;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human prostate cancer antigen #3.
 XX
 KM Immunosuppressive; neotropic; neuroprotective; antiviral; vulnerable;
 KM anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant;

KM Immune disorder; cardiovascular disorder; neurological disease;
 KM infection; cancer; cytostatic; antiarthritic; antirheumatic;
 KM antileptomatic; anticonvulsant; vasotropic; vulnery; human;
 KM secreted protein; prostate cancer antigen.
 OS Homo sapiens.
 XX
 PN WO200107476-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 20-JUL-2000; 2000WO-US19666.
 XX
 PR 21-JUL-1999; 99US-0144972.
 PR 13-AUG-1999; 99US-0148681.
 PR 17-AUG-1999; 99US-0149173.
 PR 06-OCT-1999; 99US-0158004.
 PR 05-APR-2000; 2000US-0194689.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 PI Rosen CA, Birse C;
 XX
 DR WPI: 2001-138554/14.
 DR N-PSDB; AAF72743.
 XX
 PT New nucleic acid molecule encoding human secreted prostate cancer
 PT antigens, useful for the diagnosis and treatment of disorders such as
 PT cancer, leukemia and autoimmune disease -
 XX
 PS Claim 11; Pages 385-386; 433pp; English.
 XX
 CC The present invention relates to human secreted prostate cancer antigen
 CC coding sequences (AAF72741-AAF72789) and proteins (AAB80273-AAB80321).
 CC The coding sequences and proteins of the present invention are useful for
 CC preventing, treating or ameliorating a medical condition; and for the
 CC diagnosis and treatment of diseases and disorders. Diseases and disorders
 CC that can be diagnosed and treated include (auto)immune diseases (e.g.
 CC graft versus host disease and rheumatoid arthritis), inflammatory and
 CC allergic disorders (e.g. asthma), hyperproliferative disorders (e.g.
 CC cancers and leukemias), cardiovascular disorders (e.g. heart attacks and
 CC arrhythmias), cerebrovascular disorders (e.g. stroke), arterial occlusive
 CC disorders (e.g. arteriosclerosis), angiogenesis related disorders (e.g.
 CC retinopathy and keloid scars), ocular disorders (e.g. glaucoma),
 CC neurological disorders (e.g. Alzheimer's, Parkinson's disease, epilepsy
 CC and Creutzfeld-Jakob disease) and infections caused by bacteria, fungi,
 CC viruses or parasites. They may also be useful for wound healing,
 CC epithelial cell proliferation, supporting cell culture, tissue
 CC regeneration, birth control and as a food additive or preservative.
 CC
 SO Sequence 183 AA:
 Query Match 53.2%; Score 800.5; DB 22; Length 183;
 Best Local Similarity 57.6%; Pred. No. 4,7e-62;
 Matches 160; Conservative 1; Mismatches 0; Indels 117; Gaps 2;
 QY 1 QENDGGRYSLTYITGSKHVEDPAPAFALGSLNDLOFFRYSKDRKSQPMGLRQVEGM 60
 DB 21 QENDGGRYSLTYITGSKHVEDPAPAFALGSLNDLOFFRYSKDRKSQPMGLRQVEGM 80
 QY 61 EDWKEDSLOKARBD--METLKDIVEYNDNSGSHVLOGRFGCEIENRRSSGAFWKYYDD 118
 DB 81 EDWKEDSLOKARBDIMETLKDIVEYNDNSGSHVLOGRFGCEIENRRSSGAFWKYYDD 140
 QY 119 GKDIENKELPAPVPPDPAQAQITKQWEAEPPYVQRAKAYLEBECPATLTKYLYKSKNI 178
 DB 141 GKDIENKELPAPVPPDPA----- 160
 QY 179 LDRQDDPSVYVTHQAEGEKKKLCLAVDFPKIDVHMTFRAGOVQPELRLGVDLHNGNG 238
 DB 161 ----- 160

QY 229 TYQSMVVAVPEQDTPAPSYCHVQSSLAQPLVPEWAS 276
 DB 161 -----APYSCHVQSSLAQPLVPEWAS 183
 RESULT 4
 ID AAY07773 standard; Protein; 171 AA.
 XX AAY07773:
 AC AAY07773:
 XX 06-JUL-1999 (first entry)
 DT
 XX
 DE Human secreted protein fragment encoded from gene 30.
 XX
 KW Human; secreted protein; prevention; treatment; protein therapy;
 KW gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder;
 KW developmental abnormality; foetal deficiency; blood disorder; lymphoma;
 KW leukemia; immune system disorder; autoimmune disease; hepatic disease;
 KW renal disease; inflammation; allergy; asthma; sepsis; diabetes; AIDS;
 KW Alzheimer's disease; cognitive disorder; schizophrenia; osteoporosis;
 KW arthritis; psoriasis; digestive; endocrine; infection.
 XX
 OS Homo sapiens.
 XX
 PN WO9909155-A1.
 XX
 PD 25-FEB-1999.
 XX
 PF 18-AUG-1998; 98WO-US17044.
 XX
 PR 16-JUN-1998; 98US-0092956.
 PR 15-JUL-1998; 98US-0092956.
 PR 19-AUG-1997; 97US-0056368.
 PR 19-AUG-1997; 97US-0056369.
 PR 19-AUG-1997; 97US-0056535.
 PR 19-AUG-1997; 97US-0056555.
 PR 19-AUG-1997; 97US-0056556.
 PR 19-AUG-1997; 97US-0056628.
 PR 19-AUG-1997; 97US-0056629.
 PR 19-AUG-1997; 97US-0056726.
 PR 19-AUG-1997; 97US-0056728.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Brewer LA, Duan R, Ebner R, Endress GA, Feng P;
 PI Florence C, Florence KA, Komatsoulis GA, Lafleur DW;
 PI Moore PA, Olsen HS, Rosen CA, Ruben SM, Shi Y, Soppet DR;
 PI Young PE;
 XX
 DR WPI: 1999-190160/16.
 DR N-PSDB; AAX37398.
 XX
 PT New isolated human genes and the secreted polypeptides they encode
 PT - useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 PS Claim 1b; Page 245-246; 280pp; English.
 XX
 CC This invention describes novel isolated human secreted proteins and
 CC their encoding nucleic acid sequences. The products of the invention
 CC are useful for preventing, treating or ameliorating medical conditions
 CC e.g. by protein or gene therapy. Also pathological conditions can be
 CC diagnosed by determining the presence or amount of expression of
 CC the new polypeptides in a sample or by determining the presence or
 CC absence of mutations in the new polynucleotides. Specific uses are
 CC described for each of the 70 polynucleotides, based on which tissues
 CC they are most highly expressed in, and include developing products for
 CC the diagnosis or treatment of cancer, tumours, neurodegenerative
 CC disorders, developmental abnormalities and foetal deficiencies, blood
 CC disorders, leukemias, diseases of the immune system, autoimmune
 CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
 CC asthma, sepsis, diabetes, Alzheimer's and cognitive disorders,

CC schizophrenia, osteoporosis, arthritis, psoriasis, digestive/endocrine
CC disorders, infections and AIDS. The human secreted proteins of the
CC invention are represented in AAY07744-Y07850 and the encoding nucleic
CC acids are represented in AAX37369-X37441.

XX Sequence 171 AA:

Query Match 52.6%; Score 791; DB 20; Length 171;
Best Local Similarity 97.3%; Pred. No. 2.9e-61;
Matches 146; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 QENQGRSLTITTYGLSKHVEDVPAPFALGSLNDLQFFRRYNSKDKRSQPMGLMROVEGM 60
DB 18 QENQGRSLTITTYGLSKHVEDVPAPFALGSLNDLQFFRRYNSKDKRSQPMGLMROVEGM 77
QY 61 EDWKEDSOLQKARED--METLKDIYEYNDNSNGSHVLOGFCGCEIENNSSGAFWKYYTD 118
DB 78 EDWKEDSOLQKAREDIFMETLKDIYEYNDNSNGSHVLOGFCGCEIENNSSGAFWKYYTD 137
QY 119 GMDYIEFNKEIPAWVPEDPAQITKQKWEA 148
DB 138 GMDYIEFNKEIPAWVPEDPAQITKQKWEA 167

RESULT 5

AAE80911
ID AAE80911 standard; protein: 274 AA.

XX AAE80911;

DT- 18-SEP-1990 (first entry)

DE Consensus sequence of peptides which constitute the alpha-1, alpha-2 and
alpha-3 regions of a class I HLA molecule.

XX HLA-A2 epitopes; extracellular domains alpha-1, alpha-2 and alpha-3.

XX Homo sapiens.

OS Location/Qualifiers

FT Region

FT Region

FT Region

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SQ Sequence 274 AA:
Query Match 34.9%; Score 525; DB 9; Length 274;
Best Local Similarity 39.8%; Pred. No. 9.6e-38;
Matches 111; Conservative 47; Mismatches 105; Indels 16; Gaps 8;

QY 6 GRYSLTITTYGLSKHVEDVPAPFALGSLNDLQFFRRYNS--KDKRSQPMGLMROVEGM 63
DB 1 GSHSMRYFTYSRGRGEPREFIAGVDDPQFFSDASAPRMEPRAPRIELEGPEY 60
QY 64 KEDSOLQKARED--REDMETLKDIYEYNDNSN-GSHVLOGFCGCEI--ENNSSGAFWKYY 116
DB 61 DREIYVAQSQTDREDLRTLRG---YNNQSEAGSHITQRRACDVGSDGLNLGXYH 117
QY 117 YDQKDYIEFNKEIPAWVPEDPAQITKQKWEAPYVORAAVLEECPATLRKYLYSK 176
DB 118 YDQKDYIALNEDLRGWTADPAQITQKWEAARV-ABQLRAYLEGTCVEMLRYLENGK 176
QY 177 NILDRQDPSPVYVYSHQAPGEKKIKCLAYDFYPKIDVHTTRAG--QVQPEELRGDYLH 234
DB 177 ETLQRADEPPTKTHVTHHPISDHEATLRCAALGFYPAEITLTWQROGEDQTDTEL-VEYRP 235
QY 235 NNGGTYSQMWVAVPPODTAPYSCHVQSSLAQPLVPM 273
DB 236 AGDGTQKAAVVPVSGEDQRTCHVQHEGLPKPLTLNM 274

RESULT 6

AAE68268
ID AAE68268 standard; Peptide: 365 AA.

XX AAE68268;

DT- 13-APR-2000 (first entry)

DE Human leukocyte antigen A2/A28 family protein SEQ ID NO:100.

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The present invention describes a recombinant DNA molecule (I) containing a sequence (Ia) that encodes an altered MHC (major histocompatibility complex) Class I determinant (II) comprising a polypeptide with alpha1, alpha2, alpha3 and beta2-microglobulin domains, in which alpha3 and beta2 are covalently linked, thorough C- and N-termini respectively, via a nucleotide spacer sequence encoding a

XX US6153408-A.
 PD¹ 28-NOV-2000.
 XX
 XX 09-JAN-1995; 9505-0370476.
 XX
 PR 15-NOV-1991; 91US-0792473.
 PR 07-SEP-1993; 93US-0117575.
 PR 05-DEC-1991; 91US-0801818.
 PR 07-JUN-1993; 93US-0072787.
 XX
 PA (INSP) INST PASTEUR.
 PA (INRM) INST NAT SANTE & RECH MEDICAL.
 PI Abastado J, Kourilsky P, Casrouge A, Ojcius D, Lone Y, Mottez E;
 DR WPI; 2001-060089/07.
 XX
 PT New altered major histocompatibility complex (MHC) class I determinant
 PT useful for eliciting an immune response and/or for immunizing against
 PT or treating diseases, for example, multiple sclerosis, AIDS, toxic
 PT shock or snake bite -
 XX
 PS Disclosure; Column 29-33; 105pp; English.
 XX
 CC - The present invention relates to a major histocompatibility complex
 CC (MHC) class I determinant, which has alpha_1 alpha_2 alpha_3 and
 CC beta2-microglobulin polypeptide domains encoded by a mammalian MHC
 CC class I locus. The MHC class I determinants are useful for activating
 CC the immune system and presenting antigens to the immune system to
 CC elicit an antigenic response. The MHC class I determinants are also
 CC useful for treating diseases, e.g. T cell mediated autoimmune disease,
 CC AIDS, lupus erythematosus, toxic shock or snake bite. The altered MHC
 CC class I determinants and compositions containing antigens bound to
 CC the determinants are useful in diagnostic applications, e.g. altered
 CC determinants may be used to target lymphocyte receptors and the
 CC resulting bound determinant can be assayed.
 XX
 50 Sequence 365 AA;

[illegible][illegible]

```

Query Match          33.9%; Score 510; DB 22; Length 93;
Best Local Similarity 98.9%; Pred. No. 4.7e-37;
Matches          92; Conservative      1; Mismatches     0; Indels      0; Gaps      0;

OY    184 PPSVVTSHQAFGEKKKLCLAYDEYPGKIDVHWTRAGOVQEPFLRGDVLHNGNGTYOSM 243
       |||||||
Db     1 PPSVVTSHQAFGEKKKLCLAYDEYPGKIDVHWTRAGEVEPELRLGDVLHNGNGTYOSM   60

OY    244 VVAVVPPODTAPYSCHVOHSSLAQPLVPMWES 276
       |||||||
Db     61 VVAVVPPODTAPYSCHVOHSSLAQPLVPMWES 93

RESULT 10
ID ABB24181 standard; Protein; 93 AA.
XX ABB24181;
AC
XX 23-JAN-2002 (first entry)
DT
XX
XX
XX Protein #6180 encoded by probe for measuring heart cell gene expression.
XX
XX
XX Human; gene expression; heart; microarray; vascular system;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease.
XX
XX Homo sapiens.
XX
XX WO200157274-A2.
PN
```

```

XX 09-AUG-2001.
PD
XX
PE 30-JAN-2001; 2001MO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
PS Claim 15; SEQ ID NO 25951; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 93 AA;

```

Query Match 33.9%; Score 510; DB 22; Length 93;
Best Local Similarity 98.9%; Pred. No. 4.7e-37;
Matches 92; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 184 PPSVVTSHQAPGEKKKIKCLAYDFYFGKIDVHMTFAGQVQPELRGVDVHNGNGTQSW 243
DB 1 PPSVVTSHQAPGEKKKIKCLAYDFYFGKIDVHMTFAGQVQPELRGVDVHNGNGTQSW 60
QY 244 VVAVPPQDTAPYSCHVQHSLSLAQPLVYPWEAS 276
DB 61 VVAVPPQDTAPYSCHVQHSLSLAQPLVYPWEAS 93

```

RESULT 11
AAM60079
ID AAM60079 standard; Protein; 93 AA.
XX
AC AAM60079;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 32184.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer.
XX
OS Homo sapiens.
XX
PN MO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001MO-US00667.

```

XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 32184; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention.
XX
SQ Sequence 93 AA;

```

Query Match 33.9%; Score 510; DB 22; Length 93;
Best Local Similarity 98.9%; Pred. No. 4.7e-37;
Matches 92; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 184 PPSVVTSHQAPGEKKKIKCLAYDFYFGKIDVHMTFAGQVQPELRGVDVHNGNGTQSW 243
DB 1 PPSVVTSHQAPGEKKKIKCLAYDFYFGKIDVHMTFAGQVQPELRGVDVHNGNGTQSW 60
QY 244 VVAVPPQDTAPYSCHVQHSLSLAQPLVYPWEAS 276
DB 61 VVAVPPQDTAPYSCHVQHSLSLAQPLVYPWEAS 93

```

RESULT 12
AAM72688
ID AAM72688 standard; Protein; 93 AA.
XX
AC AAM72688;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32994.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; Leukaemia; lymphoma; myeloma.
XX
OS Homo sapiens.
XX
PN MO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001MO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-488900/53.
DR
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
PS Example 4; SEQ ID NO: 32994; 658bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention.
XX
SQ Sequence 93 AA:
Query Match 33.9%; Score 510; DB 22; Length 93;
Best Local Similarity 98.9%; Pred. No. 4.7e-37;
Matches 92; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 184 PPSVVTSHQAPGEEKKIKLCLAYDFPKIDVHMTFRAGOVPELRGDLVHNGNGTQSW 243
DB 1 PPSVVTSHQAPGEEKKIKLCLAYDFPKIDVHMTFRAGEVDEPLRGDLVHNGNGTQSW 60
QY 244 VVAVVPDPTAPYSCHVOHSSLAQPLVVPWEAS 276
DB 61 VVAVVPDPTAPYSCHVOHSSLAQPLVVPWEAS 93
RESULT 13
AAM32919
ID AAM32919 standard; Protein; 93 AA.
XX
AC AAM32919;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #6956 encoded by probe for measuring placental gene expression.
XX
KW Probe: microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-48897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX
PS Claim 27; SEQ ID No 33188; 654bp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENPs

CC see AAI33315-AI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
XX
SQ Sequence 93 AA:
Query Match 33.9%; Score 510; DB 22; Length 93;
Best Local Similarity 98.9%; Pred. No. 4.7e-37;
Matches 92; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 184 PPSVVTSHQAPGEEKKIKLCLAYDFPKIDVHMTFRAGOVPELRGDLVHNGNGTQSW 243
DB 1 PPSVVTSHQAPGEEKKIKLCLAYDFPKIDVHMTFRAGEVDEPLRGDLVHNGNGTQSW 60
QY 244 VVAVVPDPTAPYSCHVOHSSLAQPLVVPWEAS 276
DB 61 VVAVVPDPTAPYSCHVOHSSLAQPLVVPWEAS 93
RESULT 14
ABG42512
ID ABG42512 standard; Peptide; 93 AA.
XX
AC ABG42512;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human peptide encoded by genome-derived single exon probe SEQ ID 32177.
XX
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tubercous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US000665.
XX
PR 04-FEB-2000; 2000US-180312P.
PR 26-MAY-2000; 2000US-207456P.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2002-114183/15.
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples -
XX
PS Claim 27; SEQ ID No 32177; 634bp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 4, 2003, 10:04:00 ; Search time 15 Seconds

(Without alignments)
541.382 Million cell updates/sec

Title: US-09-701-463-1

Perfect score: 1504

Sequence: 1 GEMQDGRYSLTYYTGLSKH.....SCHVGHSLAQPLVPWEAS 276

Scoring table: BLOSUM62

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525	34.9	274	1	US-08-222-851-1
2	511	34.0	365	2	US-08-484-905-100
3	511	34.0	365	3	US-08-481-985B-100
4	511	34.0	365	4	US-08-370-476-100
5	507	33.7	365	2	US-08-484-905-98
6	507	33.7	365	2	US-08-484-905-102
7	507	33.7	365	3	US-08-481-985B-98
8	507	33.7	365	3	US-08-481-985B-102
9	507	33.7	365	4	US-08-370-476-98
10	507	33.7	365	4	US-08-370-476-102
11	505	33.6	365	2	US-08-484-905-101
12	505	33.6	365	3	US-08-481-985B-101
13	505	33.6	365	4	US-08-370-476-101
14	504	33.5	365	2	US-08-484-905-104
15	504	33.5	365	3	US-08-481-985B-104
16	504	33.5	365	4	US-08-370-476-104
17	503	33.4	365	2	US-08-484-905-108
18	503	33.4	365	3	US-08-481-985B-108
19	503	33.4	365	4	US-08-370-476-108
20	503	33.4	365	2	US-08-484-905-97
21	503	33.4	365	3	US-08-484-905-103
22	503	33.4	365	3	US-08-481-985B-97
23	503	33.4	365	3	US-08-481-985B-103
24	503	33.4	365	4	US-08-370-476-97
25	503	33.4	365	4	US-08-370-476-103
26	500	33.2	274	4	US-08-484-905-107
27	500	33.2	274	3	US-08-481-985B-107

28	500	33.2	274	4	US-08-370-476-107	Sequence 107, App
29	497	33.0	274	2	US-08-484-905-106	Sequence 106, App
30	497	33.0	274	3	US-08-481-985B-106	Sequence 106, App
31	497	33.0	274	4	US-08-370-476-106	Sequence 106, App
32	497	33.0	365	3	US-08-652-265-23	Sequence 23, App1
33	497	33.0	365	4	US-08-834-497A-23	Sequence 23, App1
34	497	33.0	365	4	US-09-503-444A-23	Sequence 23, App1
35	492	32.7	341	3	US-08-890-719-38	Sequence 38, App1
36	492	32.7	365	2	US-08-484-905-99	Sequence 99, App1
37	492	32.7	365	3	US-08-481-985B-99	Sequence 99, App1
38	492	32.7	365	4	US-08-370-476-99	Sequence 99, App1
39	491	32.6	348	3	US-08-652-265-6	Sequence 6, App1
40	491	32.6	348	4	US-08-834-497A-6	Sequence 6, App1
41	491	32.6	348	4	US-09-503-444A-6	Sequence 6, App1
42	490	32.6	274	2	US-08-484-905-105	Sequence 105, App
43	490	32.6	274	3	US-08-481-985B-105	Sequence 105, App
44	490	32.6	274	4	US-08-370-476-105	Sequence 105, App
45	490	32.6	348	3	US-08-652-265-2	Sequence 2, App1

ALIGNMENTS

```
RESULT 1
US-08-222-851-1
; Sequence 1, Application US/08222851
; Patent No. 5723128
; GENERAL INFORMATION:
; APPLICANT: CLAYBERGER, CAROL A.
; APPLICANT: KRENSKY, ALAN M.
; APPLICANT: PARHAM, PETER
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,851
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 28600-20200.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 494-0792
; TELEX: 90-4030 MRSNFOERSM
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-222-851-1
;
; Query Match 34.9%; Score 525; DB 1; Length 274;
; Best Local Similarity 39.8%; Pred. No. 1e-41;
; Matches 111; Conservative 47; Mismatches 105; Indels 16; Gaps 8;
;
; Oy 6 GRYSLTYITGLSKHVEDVPALGSLNDIQFRYNS--KDRKSQPGMLRGVGEHMDW 63
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; Db 1 GSHSMRYFTYSVSRPGEGEPFIAVGVDPTQFVRFSDAASPRMBRAVWIEQGEPEW 60
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Best Local Simil.

Best Local Similarity 39.08; Pred. No. 3.2e-40;

Best Local Similarity 39.08; Pred. No. 3.2e-40;


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; FILING DATE: 07-SEP-1993
; APPLICATION NUMBER: US 08/072,787
; FILING DATE: 06-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05243.0001-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-370-476-98
```

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Query Match          33.7%; Score 507; DB 4; Length 365;
Best Local Similarity 38.7%; Pred. NO. 7.7e-40;
Matches 109; Conservative 47; Mismatches 110; Indels 16; Gaps 8;
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QY 6 GRYSLTYITGLSKHVEVPFAQALGSLNDLQFFRYNS--KDRKSQPMGLMROVGEWDM 63
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 25 GSHSRHYITSTSRGRGEPRIANGYDDIQFVRFDDAASQRMPEAPAPIEDGGEY 84
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 KEDSLOKA-----REDMETLKDIYEYNDN-GSHVLQGRFGCEIENN-RSSGAFWKY 116
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 85 DGEFRKVAHSGTHHVDLSTLRG---YNNQSEAGSHVQRMWGCDVSGDMFRLNGHOYA 141
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 YDKGYIFENKEIPAWPFEDPAQITTKQKWEAPYVYORAKAYLEBEPATLRKLYK 176
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 142 YDKGYIALKEDLRKMTAADMAAQTTKKWEAAHV-ASQLRAYLEGTCEWMLRRYLE 200
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 NILDRQDPSPVYVTSHPAPEGKKIKCLAYDFYPGKIDVHMTAG--OVQEPRLRGD 234
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 201 ETLQRTDAPKRTMTHHVAHSDHEATLRCAWLSFYRAEITLTWQRGEGDQTDTEL-VE 259
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 235 NGNGTYSQSVVAVVPQDTAPYSCVHQSLSLAQPLVVPWEAS 276
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 260 AGDGTFRKMAAVVPSGQEQRYTCHVQHEGLPKPLLPWEPS 301
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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```

RESULT 10
US-08-370-476-102
; Sequence 102; Application US/08370476
; Patent No. 6153408
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; APPLICANT: Lone, Xu-Chun
; APPLICANT: Ojcius, David
; APPLICANT: Castouge, Armada
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,476
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117,575
; FILING DATE: 07-SEP-1993
; APPLICATION NUMBER: US 08/072,787
; FILING DATE: 06-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05243.0001-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-370-476-102
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Query Match          33.7%; Score 507; DB 4; Length 365;
Best Local Similarity 39.3%; Pred. NO. 7.7e-40;
Matches 112; Conservative 42; Mismatches 109; Indels 22; Gaps 9;
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QY 6 GRYSLTYITGLSKHVEVPFAQALGSLNDLQFFRYNS--KDRKSQPMGLMROVGEWDM 63
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DB 25 GSHSRHYITSTSRGRGEPRIANGYDDIQFVRFDDAASQRMPEAPAPIEDGGEY 84
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 KED-----SLOKAREDMETLKDIYEYNDN-GSHVLQGRFGCEIENN-RSSGAFWKY 116
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 85 DNRNRNVAQSGQTDRLVDLSTLRG---YNNQSEAGSHIQRYGCDV---GPDGRFLNGYR 138
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 ---YDKGYIFENKEIPAWPFEDPAQITTKQKWEAPYVYORAKAYLEBEPATLRKLYK 173
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 139 QDAVDGMDYIALKEDLRKMTAADMAAQTTKKWEAAHV-AEOWRAYLEGTCEWMLRRYLE 197
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 174 YSKNILDRQDPSPVYVTSHPAPEGKKIKCLAYDFYPGKIDVHMTAG--OVQEPRLRGD 231
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 198 NKGTELQRTDAPKRTMTHHVAHSDHEATLRCAWLSFYRAEITLTWQRGEGDQTDTEL-VE 256
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 VLNHNGTYSQSVVAVVPQDTAPYSCVHQSLSLAQPLVVPWEAS 276
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 257 TRPADGTFRKMAAVVPSGQEQRYTCHVQHEGLPKPLLPWEPS 301
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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```

RESULT 11
US-08-484-905-101
; Sequence 101; Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 700
```

```

1      CITY: Washington
2      STATE: D.C.
3      ZIP: 20005-3315
4
5      COMPUTER READABLE FORM:
6      MEDIUM TYPE: Floppy Disk
7      COMPUTER: IBM PC compatible
8      OPERATING SYSTEM: PC-DOS/MS-DOS
9      SOFTWARE: PatentIn Release #1.0, Version
10
11     CURRENT APPLICATION DATA:
12     APPLICATION NUMBER: US/08/484,905
13     FILING DATE: 07-JUNE-1995
14     CLASSIFICATION: 530
15
16     PRIOR APPLICATION DATA:
17     APPLICATION NUMBER: US 07/801,818
18     FILING DATE: 05-DEC-1991
19     CLASSIFICATION: 530
20
21     PRIOR APPLICATION DATA:
22     APPLICATION NUMBER: US 07/792,473
23     FILING DATE: 15-NOV-1991
24     CLASSIFICATION: 530
25
26     ATTORNEY/AGENT INFORMATION:
27     NAME: Potter, Jane E. R.
28     REGISTRATION NUMBER: 33,332
29     REFERENCE/DOCKET NUMBER: 03495.0106-03000
30
31     TELECOMMUNICATION INFORMATION:
32     TELEPHONE: 202-408-4000
33     TELEFAX: 202-408-4400
34
35     INFORMATION FOR SEQ ID NO: 101:
36     SEQUENCE CHARACTERISTICS:
37     LENGTH: 365 amino acids
38     TYPE: amino acid
39     TOPOLOGY: linear
40
41     MOLECULE TYPE: peptide
42
43     US-08-484-905-101

```

```
;; TITLE OF INVENTION: Altered Major Histocompatibility Complex
;;
;; NUMBER OF SEQUENCES: 127
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington
;; STATE: D.C.
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/370,476
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/117,575
;; FILING DATE: 07-SEP-1993
;; APPLICATION NUMBER: US 08/072,787
;; FILING DATE: 06-JUN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/801,818
;; FILING DATE: 05-DEC-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/792,473
;; FILING DATE: 15-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Kenneth J.
;; REGISTRATION NUMBER: 25,146
;; REFERENCE/DOCKET NUMBER: 05243.0001-01000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-408-4000
;; TELEFAX: 202-408-4000
;; INFORMATION FOR SEQ ID NO: 101:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 365 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-370-476-101
```

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Query Match 33.6%; Score 505; DB 4; Length 365;
Best Local Similarity 38.2%; Pred. No. 1.2e-39;
Matches 110; Conservative 44; Mismatches 106; Indels 28; Gaps 9;

QY 6 GRYSLTYITGLSKHVEDVPFAQALGSLNDLOFFRYNS--KDRKSQPMGLMROVGEKMDW 63
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DB 25 GSHSRRYFTYSRGRGPRFRIAGYVDDTQFVRFSDASARRMRPRAFWIEOGSPETW 84
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 64 KESOLOKA----REDMETLKDIEVEYNDN-GSHVLQGRGCEIENNRSSGAFMK--- 114
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DB 85 DGETRVKVAHNSQTHVDLSTLGR---YNNQSEAGSHLVQRMGCDV-----GDMRFLR 135
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QY 115 ----YVVGKDVIEFNKEIPAWVPDPAAQITKQWEAEVYVVOAKAYLEECATLTKR 170
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DB 136 GYHQIAYDKDIALKEDLRSTADMAAQITKHKMETAHV-AEQRAYLEGTCEWLRRLR 194
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 171 YLKSNIILDRDPPSVVVTSHQAGEKKKLCLAYDTPYRGTIDVHWTRAG--QVQEPRL 228
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 195 YLENGKETLQRTDAPKTHNTNHAUSDHEATLRCWALSTFPRAETITLWDRGDDOTDTEL 254
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 229 KGDVILNGSTQSWVVAVPPDTPARYSCHVQHSLSLAQPLVVPWEAS 276
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 255 -VETPRAGDGTQKMAVAVVPSGQEQRYTCHVQHGGELPKPLTPWEPS 301
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RESULT 14
US-08-484-905-104
; Sequence 104, Application US/08484905

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;; Patent No. 5976551
;; GENERAL INFORMATION:
;; APPLICANT: Moltz, Estelle
;; APPLICANT: Adastado, Jean-Pierre
;; APPLICANT: Kourilsky, Philippe
;; TITLE OF INVENTION: An Altered Major Histocompatibility
;; TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
;; TITLE OF INVENTION: Determinant
;; NUMBER OF SEQUENCES: 127
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington
;; STATE: D.C.
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy Disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/484,905
;; FILING DATE: 07-JUNE-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/801,818
;; FILING DATE: 05-DEC-1991
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/792,473
;; FILING DATE: 15-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Potter, Jane E. R.
;; REGISTRATION NUMBER: 33,332
;; REFERENCE/DOCKET NUMBER: 03495.0106-03000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-408-4000
;; TELEFAX: 202-408-4400
;; INFORMATION FOR SEQ ID NO: 104:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 365 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-484-905-104
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Query Match 33.5%; Score 504; DB 2; Length 365;
Best Local Similarity 39.3%; Pred. No. 1.5e-39;
Matches 112; Conservative 42; Mismatches 109; Indels 22; Gaps 9;

QY 6 GRYSLTYITGLSKHVEDVPFAQALGSLNDLOFFRYNS--KDRKSQPMGLMROVGEKMDW 63
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DB 25 GSHSRRYFTYSRGRGPRFRIAGYVDDTQFVRFSDASQRMPEAPRAFWIEOGSPETW 84
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 64 -----KESOLOKAREDEMETLKDIEVEYNDN-GSHVLQGRGCEIENNRSSGAFMKY- 116
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DB 85 DENTRVKVAQSDTVDLSTLGR---YNNQSEAGSHITQIMMGCDV---GSDGRFLRGYR 138
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 117 ---YDGKDVIEFNKEIPAWVPDPAAQITKQWEAEVYVVOAKAYLEECATLTKRYLX 173
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 139 QDAYGKVDIALKEDLRSTADMAAQITKHKMEAAHV-AEQRAYLEGTCEWLRRLR 197
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 174 YKSNILDRDPPSVVVTSHQAGEKKKLCLAYDTPYRGTIDVHWTRAG--QVQEPRL 231
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 198 NGETLQRTDAPKTHNTNHAUSDHEATLRCWALSTFPRAETITLWDRGDDOTDTEL-VE 256
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 232 VILNGSTQSWVVAVPPDTPARYSCHVQHSLSLAQPLVVPWEAS 276
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 257 TRPADGDTQKMAVAVVPSGQEQRYTCHVQHGGELPKPLTPWEPS 301
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RESULT 15
US-08-481-985B-104
; Sequence 104, Application US/08481985B
; Patent No. 6011146
ORIGINAL INFORMATION

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2003, 10:04:46 ; Search time 12 Seconds
(Without alignments)
509.894 Million cell updates/sec

Title: US-09-701-463-1

Perfect score: 1504
Sequence: 1 QENQDGRSLTYITGLSKH.....SCHVHSSLAQLVLPWMEAS 276

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*
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12: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	910	60.5	170	10	US-09-925-301-1307
2	510	33.9	93	10	US-09-864-761-39479
3	492	32.7	280	9	US-10-073-300-6
4	492	32.7	415	9	US-10-073-300-5
5	465	30.9	92	10	US-09-864-761-39888
6	459	30.5	332	10	US-09-870-521-3
7	391	26.0	334	10	US-09-870-521-4
8	372	24.7	271	10	US-09-925-301-1431
9	319.5	21.2	184	9	US-09-858-580-21
10	319.5	21.2	184	9	US-09-847-172-21
11	235.5	15.7	145	10	US-09-810-560-8
12	222	14.8	78	10	US-09-864-761-39405
13	207	13.8	92	9	US-10-016-634A-120
14	205.5	13.7	110	9	US-09-796-692-799
15	204.5	13.6	110	9	US-09-796-692-2139
16	204.5	13.6	500	9	US-09-766-378A-25
17	196.5	13.1	411	9	US-10-015-536-17
18	194	12.9	353	10	US-09-815-837-92
19	192	12.8	772	10	US-09-815-837-74

20	190	12.6	547	10	US-09-815-837-90	Sequence 90, Appl
21	190	12.6	553	10	US-09-815-837-50	Sequence 50, Appl
22	190	12.6	555	10	US-09-815-837-71	Sequence 71, Appl
23	190	12.6	559	10	US-09-815-837-96	Sequence 96, Appl
24	190	12.6	560	10	US-09-815-837-73	Sequence 73, Appl
25	190	12.6	562	10	US-09-815-837-70	Sequence 70, Appl
26	190	12.6	676	10	US-09-815-837-69	Sequence 69, Appl
27	190	12.6	678	10	US-09-815-837-68	Sequence 68, Appl
28	190	12.6	774	10	US-09-815-837-72	Sequence 72, Appl
29	182.5	12.1	285	10	US-09-756-983-3	Sequence 24, Appl
30	179.5	11.9	91	10	US-09-864-761-38005	Sequence 38005, A
31	176.5	11.7	91	10	US-09-864-761-35461	Sequence 35461, A
32	175	11.6	104	10	US-09-925-302-835	Sequence 835, Appl
33	169.5	11.3	261	9	US-09-925-664-30	Sequence 30, Appl
34	166.5	11.1	441	12	US-10-081-281-115	Sequence 115, Appl
35	164.5	10.9	106	12	US-10-081-281-113	Sequence 113, Appl
36	162.5	10.8	448	12	US-10-081-281-111	Sequence 111, Appl
37	161.5	10.7	104	12	US-10-081-281-107	Sequence 107, Appl
38	161.5	10.7	117	10	US-09-810-560-9	Sequence 9, Appl
39	152.5	10.1	181	10	US-09-925-302-515	Sequence 515, Appl
40	150.5	10.0	174	9	US-10-079-623-356	Sequence 356, Appl
41	139	9.2	272	10	US-09-925-301-855	Sequence 855, Appl
42	137.5	9.1	246	9	US-09-992-598-225	Sequence 225, Appl
43	137.5	9.1	246	9	US-09-989-735-225	Sequence 225, Appl
44	137.5	9.1	246	9	US-09-989-735-225	Sequence 225, Appl
45	137.5	9.1	246	9	US-09-990-444-225	Sequence 225, Appl

ALIGNMENTS

```
RESULT 1
US-09-925-301-1307
; Sequence 1307, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925, 301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124, 270
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 1307
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1307

Query Match      60.5%; Score 910; DB 10; Length 170;
Best Local Similarity 99.4%; Pred. No. 3.6e-69;
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 112 FWKYYGKDYIEFNKTIIPAWPPDPRAQITKQWEAEPPYVORAKAYLEECPATIRKY 171
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DB 6 FWKYYGKDYIEFNKTIIPAWPPDPRAQITKQWEAEPPYVORAKAYLEECPATIRKY 65

QY 172 LKYSKNLIDDDPPSVVTSVTHQAGKKKTKCLAYDPKPIDVHMTACOVQPEPLRGD 231
      |||||||
DB 66 LKYSKNLIDDDPPSVVTSVTHQAGKKKTKCLAYDPKPIDVHMTACOVQPEPLRGD 125

QY 232 VLHNGNGTYSWVAVVPDPTAPYSCVHSSLAQLVLPWMEAS 276
      |||||||
DB 126 VLHNGNGTYSWVAVVPDPTAPYSCVHSSLAQLVLPWMEAS 170

RESULT 2
US-09-864-761-39479
; Sequence 39479, Application US/09864761
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Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmiga-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 39479
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004977.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.79
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 16
; OTHER INFORMATION: SWISSPROT HIT: P25311, EVALU 5.00e-53
US-09-864-761-39479
Query Match 33.9%; Score 510; DB 10; Length 93;
Best Local Similarity 98.9%; Pred. No. 4.5e-36;
Matches 92; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 244 VVAVPDDTAAYSCHVQHSLSLAQPLVYPWEAS 276
Db 61 VVAVPDDTAAYSCHVQHSLSLAQPLVYPWEAS 93
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; Sequence 6, Application US/10073300
; Publication No. US20030003535A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES
; FILE REFERENCE: 02/23339
; CURRENT APPLICATION NUMBER: US/10/073,300
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-073-300-6

Query Match 32.7%; Score 492; DB 9; Length 280;
Best Local Similarity 37.9%; Pred. No. 5.7e-34;
Matches 107; Conservative 48; Mismatches 111; Indels 16; Gaps 8;
QY 6 GRYSLIYITGLSKHVEDYPAFOALGSLNDLOFFRYNS--KDRKSQPMGLMRQVGMEDW 63
Db 1 GSHSMRYFTTSVRGGRGPRFIAVGYDDDTQFVAFSDAASQMRPAPWIECGPEYW 60
QY 64 KEDSOLQRA----REDMETLKDIYEYNDNS-GSHVLOGRGCEIENN-RSSGAFMYX 116
Db 61 DEETKRVKNAHSQTHRYVDLGLTNG--YYNQSEAGSHTYQRMGCDVGDWRLRGYHOYA 117
QY 117 YDGKRYIEFNKEIPAWVPEDPAOITKOKMEAPYVORAKAYLEECPATLRKYLYTSK 176
Db 118 YDGKRYIEFNKEIPAWVPEDPAOITKOKMEAPYVORAKAYLEECPATLRKYLYTSK 176
QY 177 NILDRDPPSVVYTSQAGGKKLCLAYDFYPKRIDVHWTRAG--GVQEPRLGVDYLH 234
Db 177 ETLQRTDAPKTHMTHTHAASVDHEATLRCWALSFPYPAEITLTWQDDEDTQDTDEL-VETRP 235
QY 235 NNGTYQSNNVAVVPDDTAAYSCHVQHSLSLAQPLVYPWEAS 276
Db 236 ADDGTGFQKMAAVVPSGQDQRYTCHVQHEGLPKPLTRWEOS 277

RESULT 4
US-10-073-300-5
; Sequence 5, Application US/10073300
; Publication No. US20030003535A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES
; FILE REFERENCE: 02/23339
; CURRENT APPLICATION NUMBER: US/10/073,300
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human beta2 microglobulin linked to MHC class I heavy chain
US-10-073-300-5

Query Match 32.7%; Score 492; DB 9; Length 415;
Best Local Similarity 37.9%; Pred. No. 9.3e-34;
Matches 107; Conservative 48; Mismatches 111; Indels 16; Gaps 8;
QY 6 GRYSLIYITGLSKHVEDYPAFOALGSLNDLOFFRYNS--KDRKSQPMGLMRQVGMEDW 63

Db	116	GSHSMRYEFTSVSRGRGEPRFIAVGYVDITQFVRFPDSDAASQMEPRAMINGEGEPEYM	175
Qy	64	KEDSOLQAK-----REMETIKOLIVETYYNDSN-GSHYLOGRFGCEIENN-RSSGAFPKYI	116
Db	176	DGETKKVAASHSOTHHVDGLTNG---YNSOEAASHVYQRRYGGDVSDMRFLTNGHYOA	232
Qy	117	YDGKDIYEENKEIPAWWFEDPAOITKQKMEAEVYVQARAKVILEEBCPATTILKKYLYKS	176
Db	233	YDGKDYILKEDLRSWTAADAAATQTHKKMEAAHV-AEOGRAVYEGTCVEMTLRYLNGK	291
Qy	177	NILRQDRPSVVVNRSHOARGKKKTLCAADYEYKQIDVMTFRAG--QVQPELPGVLIH	234
Db	292	ETLQRTQARKNTHMHNHVAHSDEALTRCMALSTFYAETLLTWMQRGEQDTDEL-VEITR	350
Qy	235	NGNGTYSQSVVVVYANPRDITAFYISCHVYQHSIAQPLVYVMEAS	276
Db	351	AGDGTFOKMAVVVPSGQEQRYTTHVYHEGILPKFLYLRMOS	392

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1      RESULT 5
2      US-09-864-761-39888
3      Sequence 39888, Application US/09864761
4      Patent No. US2002048763A1
5      GENERAL INFORMATION:
6      APPLICANT: Penn, Sharon G.
7      APPLICANT: Rank, David R.
8      APPLICANT: Hanzel, David K.
9      APPLICANT: Chen, Weisheng
10     TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
11     FILE REFERENCE: Aecmica-X-1
12     CURRENT FILING DATE: 2001-05-23
13     PRIOR APPLICATION NUMBER: US/09/864,761
14     PRIOR FILING DATE: 2000-02-04
15     PRIOR APPLICATION NUMBER: US 60/207,456
16     PRIOR FILING DATE: 2000-05-26
17     PRIOR APPLICATION NUMBER: US 09/632,366
18     PRIOR FILING DATE: 2000-08-03
19     PRIOR APPLICATION NUMBER: GB 24263.6
20     PRIOR FILING DATE: 2000-10-04
21     PRIOR APPLICATION NUMBER: US 60/236,359
22     PRIOR FILING DATE: 2000-09-27
23     PRIOR APPLICATION NUMBER: PCT/US01/00666
24     PRIOR FILING DATE: 2001-01-30
25     PRIOR APPLICATION NUMBER: PCT/US01/00667
26     PRIOR FILING DATE: 2001-01-30
27     PRIOR APPLICATION NUMBER: PCT/US01/00664
28     PRIOR FILING DATE: 2001-01-30
29     PRIOR APPLICATION NUMBER: PCT/US01/00669
30     PRIOR FILING DATE: 2001-01-30
31     PRIOR APPLICATION NUMBER: PCT/US01/00665
32     PRIOR FILING DATE: 2001-01-30
33     PRIOR APPLICATION NUMBER: PCT/US01/00668
34     PRIOR FILING DATE: 2001-01-30
35     PRIOR APPLICATION NUMBER: PCT/US01/00663
36     PRIOR FILING DATE: 2001-01-30
37     PRIOR APPLICATION NUMBER: PCT/US01/00662
38     PRIOR FILING DATE: 2001-01-30
39     PRIOR APPLICATION NUMBER: PCT/US01/00661
40     PRIOR FILING DATE: 2001-01-30
41     PRIOR APPLICATION NUMBER: PCT/US01/00670
42     PRIOR FILING DATE: 2001-01-30
43     PRIOR APPLICATION NUMBER: US 60/234,687
44     PRIOR FILING DATE: 2000-09-21
45     PRIOR APPLICATION NUMBER: US 09/608,408
46     PRIOR FILING DATE: 2000-06-30
47     PRIOR APPLICATION NUMBER: US 09/774,203
48     PRIOR FILING DATE: 2001-01-29
49     NUMBER OF SEQ ID NOS: 49117
50     SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
51     SEQ ID NO 39888

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[illegible]


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: PRIOR FILING DATE: 2000-03-17
: PRIOR APPLICATION NUMBER: 60/200,545
: PRIOR FILING DATE: 2000-04-27
: PRIOR APPLICATION NUMBER: 60/200,303
: PRIOR FILING DATE: 2000-04-28
: PRIOR APPLICATION NUMBER: 60/200,779
: PRIOR FILING DATE: 2000-04-28
: PRIOR APPLICATION NUMBER: 60/200,999
: PRIOR FILING DATE: 2000-05-01
: PRIOR APPLICATION NUMBER: 60/202,084
: PRIOR FILING DATE: 2000-05-04
: PRIOR APPLICATION NUMBER: 60/206,201
: PRIOR FILING DATE: 2000-05-22
: PRIOR APPLICATION NUMBER: 60/223,378
: PRIOR FILING DATE: 2000-05-22
: PRIOR APPLICATION NUMBER: 60/218,950
: PRIOR FILING DATE: 2000-07-14
: PRIOR APPLICATION NUMBER: 60/222,903
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: 60/223,416
: PRIOR FILING DATE: 2000-08-04
: PRIOR APPLICATION NUMBER: 60/223,378
: PRIOR FILING DATE: 2000-08-07
: NUMBER OF SEQ ID NOS: 9597
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 799
: LENGTH: 110
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-796-692-799

Query Match          13.7%  Score 205.5;  DB 9;  Length 110;
Best Local Similarity 41.0%;  Pred. No. 1.6e-10;
Matches 43;  Conservative 17;  Mismatches 42;  Indels 3;  Gaps 2;

Cy      126  NKEIYAWPFPQAQITKQKEAPEYVYQAKAYLEECPATLTKYLSKNIIRDPP 185
      ::::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
      ::::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      3    NEDLRSWNADMAQITRKWEAAH-EAEQRAYIDGTCVWMLBRYLLENGKETLQRDPP 61
      ::::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
      ::::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

Cy      186  SVVYTSHQAPGEEKKLCCLAYDFYPGKIDVWITAG--QVQPEPL 228
      ::::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
      ::::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      62  KHTMTHPISDHEATLRCMALGFYPAETITWQRDGEDQDQDTDEL 106
      ::::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 15
US-09-796-692-2139
: Sequence 2139, Application US/09796692
: Publication No. US20020198362A1
: GENERAL INFORMATION:
: APPLICANT: Gaiger, Alexander
: APPLICANT: Algate, Paul A.
: APPLICANT: Mannion, Jane
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
: FILE REFERENCE: 2077_001200
: CURRENT APPLICATION NUMBER: US/09/796,692
: PRIOR APPLICATION NUMBER: 60/186,126
: PRIOR FILING DATE: 2000-03-01
: PRIOR APPLICATION NUMBER: 60/190,479
: PRIOR FILING DATE: 2000-03-17
: PRIOR APPLICATION NUMBER: 60/200,545
: PRIOR FILING DATE: 2000-04-27
: PRIOR APPLICATION NUMBER: 60/200,303
: PRIOR FILING DATE: 2000-04-28
: PRIOR APPLICATION NUMBER: 60/200,779
: PRIOR FILING DATE: 2000-04-28
: PRIOR APPLICATION NUMBER: 60/200,999
: PRIOR FILING DATE: 2000-05-01
: PRIOR APPLICATION NUMBER: 60/202,084
: PRIOR FILING DATE: 2000-05-04
: PRIOR APPLICATION NUMBER: 60/206,201
: PRIOR FILING DATE: 2000-05-22
: PRIOR APPLICATION NUMBER: 60/218,950
: PRIOR FILING DATE: 2000-07-14

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 4, 2003, 10:03:40 ; Search time 18 Seconds

(Without alignments)
1474.061 Million cell updates/sec

Title: US-09-701-463-1

Perfect score: 1504

Sequence: 1 OENQDGRYSLTLYTGSKH.....SCHVQSSLAQLPVPEAS 276

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1487	98.9	298	2	A54175
2	901	59.9	279	2	JX0353
3	877	58.3	290	2	JX0352
4	527	35.0	362	1	HLH087
5	527	35.0	362	2	I59651
6	525	34.9	362	2	I37515
7	524	34.8	362	2	I61865
8	522	34.7	362	2	S60601
9	521	34.6	355	2	I80169
10	519	34.5	354	2	S18197
11	519	34.5	362	2	JH0538
12	518	34.4	354	2	I80165
13	518	34.4	365	2	I36961
14	518	34.4	365	2	I54493
15	517	34.4	338	2	I56116
16	517	34.4	362	2	I68724
17	517	34.4	365	2	S77963
18	517	34.4	365	2	I54416
19	516	34.3	354	2	I80167
20	515	34.2	361	2	B27658
21	515	34.2	362	1	HLH082
22	514	34.2	361	2	I54418
23	514	34.2	362	2	I72755
24	513	34.1	362	2	I59645
25	512	34.0	362	2	I54298
26	511	34.0	332	2	S06424
27	511	34.0	362	2	I68850
28	510	33.9	362	2	I72753
29	510	33.9	362	2	I56130

30	510	33.9	362	2	I81233	Lymphocyte antigen
31	509	33.8	350	2	I68747	MHC class I lympho
32	509	33.8	362	2	I84431	MHC HLA-B8 chain -
33	509	33.8	365	2	A47636	MHC class I histoc
34	509	33.8	365	2	I83063	HLA-B*5601 - human
35	508	33.8	355	2	I80171	HLA-B*5601 - human
36	508	33.8	358	2	S03538	MHC class I histoc
37	508	33.8	362	2	I72754	MHC class I histoc
38	508	33.8	362	2	I36962	MHC class I protei
39	508	33.8	362	2	I56133	MHC class I protei
40	508	33.8	362	2	I54314	MHC HLA-B39N - hum
41	508	33.8	362	2	I61904	MHC class I histoc
42	508	33.8	363	2	S03537	MHC class I histoc
43	507	33.7	362	2	C35997	MHC class I histoc
44	507	33.7	362	2	I54505	Lymphocyte antigen
45	507	33.7	365	2	S01171	class I histocompa

ALIGNMENTS

RESULT 1
A54175
zinc-alpha-2-glycoprotein precursor - human
N:Alternate names: class I histocompatibility complex alpha chain homolog
C:Species: Homo sapiens (man)
C:Date: 13-Sep-1994 #sequence revision 18-Nov-1994 #text change 24-Nov-1999
C:Accession: A54175; A49357; I52248; S17564; A31080; PC2210; I65208; J00946
R:Ueyama, H.; Deng, H.X.; Ohkubo, I.
Biochemistry 32, 12968-12976, 1993
A:Title: Molecular cloning and chromosomal assignment of the gene for human Zn-alpha
A:Reference number: A54175; MUID:94059971; PMID:8241150
A:Accession: A54175
A:Molecule type: DNA
A:Residues: 1-298 <DEX1>
A:Cross-references: GB:D14034; NID:9456585
A:Note: sequence extracted from NCBI backbone (NCBI:140118, NCBI:140119)
R:Freije, J.P.; Fuenyo, A.; Uribe, J.A.; Velasco, G.; Sanchez, L.M.; Lopez-Boado, Y.S.;
Genomics 18, 575-587, 1993
A:Title: Human Zn-alpha-2-glycoprotein: complete genomic sequence, identification of
A:Reference number: A49357; MUID:94140356; PMID:8307568
A:Accession: A49357
A:Molecule type: DNA
A:Residues: 1-298 <PRE>
A:Cross-references: GB:X69953; NID:9467670; PIDN:CAA49574.1; PID:9467671
R:Ueyama, H.; Niwa, M.; Tada, T.; Sasaki, M.; Ohkubo, I.
Biochem. Biophys. Res. Commun. 177, 656-703, 1991
A:Title: Cloning and nucleotide sequence of a human Zn-alpha2-glycoprotein cDNA and c
A:Reference number: I52248; MUID:91264833; PMID:2049092
A:Accession: I52248
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 4-298 <DEX2>
A:Cross-references: GB:D90427; NID:9220150; PIDN:BAA14417.1; PID:9220151; GB:M76707;
A:Note: submitted to JRPD, June 1991
R:Freije, J.P.; Fuenyo, A.; Uribe, J.; Lopez-Otin, C.
FEBS Lett. 290, 247-249, 1991
A:Title: Human Zn-alpha(2)-glycoprotein cDNA cloning and expression analysis in benign
A:Reference number: S17564; MUID:92008677; PMID:1915885
A:Accession: S17564
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-298 <PRE>
A:Cross-references: EMBL:X59766; NID:938025; PIDN:CAA42438.1; PID:938026
R:Araki, T.; Gejyo, F.; Takagaki, K.; Haupt, H.; Schwick, H.G.; Buergli, W.; Marti, T.
Proc. Natl. Acad. Sci. U.S.A. 85, 679-683, 1988
A:Title: Complete amino acid sequence of human plasma Zn-alpha-2-glycoprotein and its
A:Reference number: A31080; MUID:88124905; PMID:3422450
A:Accession: A31080
A:Molecule type: protein
A:Residues: 21-84, 'E', '86-95, '98-243, 'Q', '245-298 <ARA>
R:Takagaki, M.; Honke, K.; Tsukamoto, T.; Higashiyama, S.; Taniguchi, N.; Makita, A.;
Biochem. Biophys. Res. Commun. 201, 1339-1347, 1994

A:Title: Zn-alpha2-glycoprotein is a novel adhesive protein.
A:Reference number: PC2210; MUID:94296408; PMID:8024578
A:Accession: PC2210
A:Molecule type: protein
A:Residues: 239-256, 'D', 258-265 <TAK>
A:Experimental source: prostate, liver
C:Genetics:
A:Gene: GDB:AZGP1; ZAGC
A:Cross-references: GDB:128308; OMIM:194460
A:Map position: 7q22.1-7q22.1
A:Introns: 26/1 113/1 205/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: extracellular protein; glycoprotein; monomer; pyroglutamic acid; zinc
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-298/Product: zinc-alpha-2-glycoprotein #status experimental <MAT>
F:251-253/Region: cell attachment (R-G-D) motif
F:21/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
F:109/Binding site: carbohydrate (Asn) (covalent) #status absent
F:112,128,259/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:123-186,225-280/Disulfide bonds: #status experimental

Query Match 98.9%; Score 1487; DB 2; Length 298;
Best Local Similarity 98.6%; Pred. No. 1.3e-105;
Matches 274; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

OY 1 QENDGRSLTYITGLSKHVEDPAPFQALGSLNDLOFFRYNSKDRKSQPMGLMROVEGM 60
DB 21 QENDGRSLTYITGLSKHVEDPAPFQALGSLNDLOFFRYNSKDRKSQPMGLMROVEGM 80
OY 61 EDWEDSOLQKARED--METLKDIVEYNDNSGSHVLOGRGCEIENNRSSGAFMKYYXD 118
DB 81 EDWEDSOLQKAREEITMETLKDIVEYNDNSGSHVLOGRGCEIENNRSSGAFMKYYXD 140
OY 119 GIDYIEFNKEIPAWPFPDPAQTOKWEAEVYVQRAKAYLEECPPATLRKYLSKNI 178
DB 141 GIDYIEFNKEIPAWPFPDPAQTOKWEAEVYVQRAKAYLEECPPATLRKYLSKNI 200
OY 179 LDRPPSVVVTSHOAPGEKKLKLCLAVDFYFGKIDVHMTAAGVQOEBELRGDVLHNGNG 238
DB 201 LDRPPSVVVTSHOAPGEKKLKLCLAVDFYFGKIDVHMTAAGVQOEBELRGDVLHNGNG 260
OY 239 TYQSNVVAVPPDPTAPYSCHVQSSLAQPLVPEWEAS 276
DB 261 TYQSNVVAVPPDPTAPYSCHVQSSLAQPLVPEWEAS 298

61N
C

RESULT 2
JX0353
zinc-alpha 2-glycoprotein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Apr-1995 #sequence_revision 26-May-1995 #text_change 11-Jan-2000
C:Accession: JX0353
R:Ueyama, H.; Naitoh, H.; Ohkubo, I.
J. Biochem. 116, 677-681, 1994
A:Title: Structure and expression of rat and mouse mRNAs for Zn-alpha 2-glycoprotein.
A:Reference number: JX0352; MUID:95155283; PMID:7852290
A:Accession: JX0353
A:Molecule type: mRNA
A:Residues: 1-279 <UEV>
A:Cross-references: DDBJ:D21058
A:Experimental source: liver
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein
F:4-90/Region: domain A
F:91-182/Region: domain B
F:183-279/Region: domain C
F:106,237/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 59.9%; Score 901; DB 2; Length 279;
Best Local Similarity 60.0%; Pred. No. 3.7e-61;
Matches 163; Conservative 39; Mismatches 65; Indels 6; Gaps 4;

OY 4 QDCGRSLTYITGLSKHVEDPAPFQALGSLNDLOFFRYNSKDRKSQPMGLMROVEGM 63.

DB 2 ETGSSYLITLYTGLSKHVEDPAPFQALGSLNDLOFFRYNSKDRKSQPMGLMROVEGM 61
OY 64 KEDSOLQKARED--METLKDIVEYNDNSGSHVLOGRGCEIENNRSSGAFMKYYIDGD 121
DB 62 EKESQOLQKAREEITMETLKDIVEYNDNSGSHVLOGRGCEIENNRSSGAFMKYYIDGD 121
OY 122 YIEFNKEIPAWPFPDPAQTOKWEAEVYVQRAKAYLEECPPATLRKYLSKNI 181
DB 122 YIEFNKEIPAWPFPDPAQTOKWEAEVYVQRAKAYLEECPPATLRKYLSKNI 181
OY 182 QDPPSVVVTSHOAPGEKKLKLCLAVDFYFGKIDVHMTAAGVQOEBELRGDVLHNGNG 239
DB 182 TDPPYKITSRVAPGRNRIIRCLAYDFPQRIISLHNMVQASKLASEPE-RG-VFPMNGT 239
OY 240 YQSNVVAVPPDPTAPYSCHVQSSLAQPLVPEWE 274
DB 240 YLSMVEVPPQNDPFCVCHIEHKGISQSLVSQMD 274

RESULT 3

JX0352
zinc-alpha 2-glycoprotein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Apr-1995 #sequence_revision 26-May-1995 #text_change 24-Nov-1999
C:Accession: JX0352; I84729
R:Ueyama, H.; Naitoh, H.; Ohkubo, I.
J. Biochem. 116, 677-681, 1994
A:Title: Structure and expression of rat and mouse mRNAs for Zn-alpha 2-glycoprotein.
A:Reference number: JX0352; MUID:95155283; PMID:7852290
A:Accession: JX0352
A:Molecule type: mRNA
A:Residues: 1-290 <UEV>
A:Cross-references: DDBJ:D21059
A:Experimental source: liver
R:Noguchi, M.; Kitabatake, A.; Ishibashi, T.; Kasahara, M.
Immunogenetics 42, 72-74, 1995
A:Title: The MHC class I-like Zn-alpha 2-glycoprotein gene maps to mouse chromosome 5
A:Reference number: I49450; MUID:95317827; PMID:7797272
A:Accession: I84729
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 218-287 <RES>
A:Cross-references: GB:D44593; NID:9995470; PID:9995471
A:Experimental source: C57BL/6J mice
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein
F:4-91/Region: domain A
F:92-182/Region: domain B
F:183-290/Region: domain C
F:106,237/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.3%; Score 877; DB 2; Length 290;
Best Local Similarity 59.3%; Pred. No. 2.6e-59;
Matches 163; Conservative 36; Mismatches 70; Indels 6; Gaps 4;

OY 4 QDCGRSLTYITGLSKHVEDPAPFQALGSLNDLOFFRYNSKDRKSQPMGLMROVEGM 63
DB 2 ETGSSYLITLYTGLSKHVEDPAPFQALGSLNDLOFFRYNSKDRKSQPMGLMROVEGM 61
OY 64 KEDSOLQKARED--METLKDIVEYNDNSGSHVLOGRGCEIENNRSSGAFMKYYIDGD 121
DB 62 EKESQOLQKAREEITMETLKDIVEYNDNSGSHVLOGRGCEIENNRSSGAFMKYYIDGD 121
OY 122 YIEFNKEIPAWPFPDPAQTOKWEAEVYVQRAKAYLEECPPATLRKYLSKNI 181
DB 122 YIEFNKEIPAWPFPDPAQTOKWEAEVYVQRAKAYLEECPPATLRKYLSKNI 181
OY 182 QDPPSVVVTSHOAPGEKKLKLCLAVDFYFGKIDVHMTAAGVQOEBELRGDVLHNGNG 239
DB 182 IDPPYKITSRVAPGRNRIIRCLAYDFPQRIISLHNMVQASKLASEPE-RG-VFPMNGT 239
OY 240 YQSNVVAVPPDPTAPYSCHVQSSLAQPLVPEWE 274

Db 240 YLSMAVEVSPQIDIDPFECFLIDHGFSGSLQVMD 274

RESULT 4

MHC class I histocompatibility antigen HLA-B7 alpha chain precursor - human
HLA-B7
C/Species: Homo sapiens (man)
C/Date: 31-Jul-1990 #sequence_revision 22-Apr-1995 #text_change 01-Dec-2000
C/Accession: B35997; A90435; A93840; I54420; I68701; A02105
R/Emis: P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
Proc. Natl. Acad. Sci. U.S.A. 87, 2833-2837, 1990
A/Title: Rapid cloning of HLA-A,B cDNA by using the polymerase chain reaction: frequency
A/Reference number: A35997; MUID:90207291; PMID:2320591
A/Accession: B35997
A/Molecule type: mRNA
A/Residues: 1-362 <ENR>
A/Cross-references: GB:M32317; NID:9187786; PIDN:AAA6230.1; PID:g307221
A/Note: this allele is designated B*0702 (previously HLA-B*7.2)
R/Orr, H.T.; Lopez de Castro, J.A.; Lancet, D.; Strominger, J.L.
Biochemistry 18, 5711-5720, 1979
A/Title: Complete amino acid sequence of a papain-solubilized human histocompatibility A
A/Reference number: A90435; MUID:80086278; PMID:518865
A/Accession: A90435
A/Molecule type: protein
A/Residues: 25-265; 'E', 267-295 <ORR>
R/Tragardh, L.; Rask, L.; Wilman, K.; Fohlman, J.; Peterson, P.A.
Proc. Natl. Acad. Sci. U.S.A. 77, 1129-1133, 1980
A/Title: Complete amino acid sequence of pooled papain-solubilized HLA-A, -B, and -C anti
A/Reference number: A93840; MUID:80145722; PMID:6928663
A/Accession: A93840
A/Molecule type: protein
A/Residues: 25-42; 'Q', 44-47; 'N', 49-53; 'N', 55-68; 'Q', 70-86; 'Q', 88-93; 'H', 95-139; 'TRAI', 14
A/Experimental source: pooled HLA-A, -B, and -C antigens
A/Note: this sequence represents the predominant amino acid at each position
R/Trapani, J.A.; Mickelson, C.A.; Deacon, N.J.; Hooker, D.J.; McKenzie, I.F.
Immunogenetics 22, 399-405, 1985
A/Title: Molecular cloning and partial nucleotide sequence of a 3.5 kb HLA-B*27-associate
A/Reference number: I54420; MUID:86032060; PMID:2997032
A/Accession: I54420
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 350-362 <RES>
A/Cross-references: GB:M15634; NID:9187661; PIDN:AAA59615.1; PID:g443670
R/Annot, D.; Lillie, J.W.; Auftray, C.; Kappes, D.; Strominger, J.L.
Immunogenetics 20, 237-252, 1984
A/Title: Inter-locus and intra-allelic polymorphisms of HLA class I antigen gene mRNA.
A/Reference number: I54412; MUID:84287690; PMID:6332068
A/Accession: I68701
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 63-93; 'H', 95-362 <RE2>
A/Cross-references: GB:M27540; NID:9187733; PIDN:AAA59638.1; PID:g386890
C/Genetics:
A/Gene: GDB:HLA-B
A/Cross-references: GDB:120048; OKIM:142830
A/Map position: 6p21.3-6p21.3
C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterodimer; surface antigen; transmembrane prote
F:1-24/Domain: signal sequence
F:25-114/Domain: alpha-1 <EX1>
F:115-206/Domain: alpha-2 <EX2>
F:220-285/Domain: immunoglobulin homology <IMM>
F:307-331/Domain: transmembrane #status predicted <TM>
F:332-362/Domain: intracellular #status predicted <INT>
F:110/binding site: carbohydrate (Asn) (covalent) #status experimental
F:125-188, 227-283/Disulfide bonds: #status experimental

Query Match 35.0%; Score 527; DB 1; Length 362;
Best Local Similarity 39.9%; Pred. No. 1,3e-32;
Matches 113; Conservative 49; Mismatches 111; Indels 10; Gaps 7;
QY 2 ENQGRYSLYITVGLSKHVEDVPAFOALGSLNDLQFFRYS--KDRSQPMGLMROVEG 59

Db 21 ETWAGSHSMRYFYTSVSPGRGEPFISVGYDDTQFVRFPDSDAASPREPRAPWTEDEG 80
QY 60 MEDWKEQSOLQK--AREDMETLKDIVEYYNDSN--GSHVLOGFGCEI--ENNRSSGAEFWKY 115
Db 81 PEYMDRNTQIYKAAQOTRRESLRNLRGYNOSEAGSHTLQSGYGDVGPDRLLRGHNOY 140
QY 116 YYDGKDYIEFNKEIPAWVPFPDPAQITQKWEAEFVYQRAKAYLEECPTATLRKYLKYS 175
Db 141 AYDGKDYIALMEDLRSMWTAADTAQITQKWEAEAREAEOR--RAYLEGCVEMLRRYLENG 199
QY 176 KNIIDRDPSPVSVTSHOAPGEKKKCLADFYFGKIDVHWTRAG--QVQEPRLRGDYL 233
Db 200 KDKLERADPPTVHTVTHHISDHEATLRKMGALGFPAETLLTWQRNGEDQTDTEL--VETR 258
QY 234 HNGNGTQSWVYVAVPPDPTAPYSCHVQHSLSLAQPLVVPWAS 276
Db 259 PAGDRTFQKMAAVVVPSCGEORVTCYHVGHEGLPKPLTLRWEPSS 301

RESULT 5

159651
Lymphocyte antigen - human
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C/Accession: I59651
R/Amelt, K.L.; Adams, E.J.; Domena, J.D.; Parham, P.
Tissue Antigens 44, 318-321, 1994
A/Title: Structure of a novel subtype of B7 (B*0705) isolated from a Chinese individu
A/Reference number: I59651; MUID:95184211; PMID:7878658
A/Accession: I59651
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-362 <RES>
A/Cross-references: GB:I33922; NID:9520834; PIDN:AAA65639.1; PID:g520835
C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 35.0%; Score 527; DB 2; Length 362;
Best Local Similarity 39.9%; Pred. No. 1,3e-32;
Matches 113; Conservative 49; Mismatches 111; Indels 10; Gaps 7;
QY 2 ENQGRYSLYITVGLSKHVEDVPAFOALGSLNDLQFFRYS--KDRSQPMGLMROVEG 59
Db 21 ETWAGSHSMRYFYTSVSPGRGEPFISVGYDDTQFVRFPDSDAASPREPRAPWTEDEG 80
QY 60 MEDWKEQSOLQK--AREDMETLKDIVEYYNDSN--GSHVLOGFGCEI--ENNRSSGAEFWKY 115
Db 81 PEYMDRNTQIYKAAQOTRRESLRNLRGYNOSEAGSHTLQSGYGDVGPDRLLRGHNOY 140
QY 116 YYDGKDYIEFNKEIPAWVPFPDPAQITQKWEAEFVYQRAKAYLEECPTATLRKYLKYS 175
Db 141 AYDGKDYIALMEDLRSMWTAADTAQITQKWEAEAREAEOR--RAYLEGCVEMLRRYLENG 199
QY 176 KNIIDRDPSPVSVTSHOAPGEKKKCLADFYFGKIDVHWTRAG--QVQEPRLRGDYL 233
Db 200 KDKLERADPPTVHTVTHHISDHEATLRKMGALGFPAETLLTWQRNGEDQTDTEL--VETR 258
QY 234 HNGNGTQSWVYVAVPPDPTAPYSCHVQHSLSLAQPLVVPWAS 276
Db 259 PAGDRTFQKMAAVVVPSCGEORVTCYHVGHEGLPKPLTLRWEPSS 301

RESULT 6
137515
MHC class I histocompatibility antigen HLA-B*2706 alpha chain precursor - human
C/Species: Homo sapiens (man)
C/Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C/Accession: I37515
R/Vilches, C.; de Pablo, R.; Kreisler, M.
Immunogenetics 39, 219, 1994
A/Title: Nucleotide sequence of HLA-B*2706.
A/Reference number: I37515; MUID:94102824; PMID:8276469

A;Residues: 1-338 <RES>
 A;Cross-references: GB:M62852; NID:q187760; PIDN:AAA59647.1; PID:q187761
 C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
 F;196-261/Domain: immunoglobulin homology <IMM>

Query Match 34.4%; Score 517; DB 2; Length 338;

Best Local Similarity 39.1%; Pred. No. 6,7e-32;

Matches 109; Conservative 48; Mismatches 112; Indels 10; Gaps 7;

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QY 6 GRYSLTIYITGLSKHVEDVPAFOALGSLNDLQFFRYS--KDRKSQPMGLMRQVEGMEDW 63
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1 GSHSMRYFHTSVSRPGRGEPRTITVGVDLTFVRFDSDAASPREPRAPWIEQEGPEYW 60

QY 64 KEDSOL--OKARDEMETLKDIVETYYNDSN--GSHVLOGRFGCEI--ENNRSQAFWKYYYG 119
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 61 DRETQICKAKAQTDREDLRTILRTYNOSEAGSHTLQSMTGCDVGPGRRLRGHNQYAYDG 120

QY 120 KDYLEFNKEIPAWVPFDPAAQITROKWEAEPPVYORAKAYLEECAPATLRKYLKYSKNIL 179
   | | | | : : | : | : | : | : | : | : | : | : | : | : | : |
Db 121 KDYLALNEDLRSWTAAADTAQITQRKWEARV--AEQLRAYLEGCEVETLRRYLENGKETL 179

QY 180 DRODPPSVVVTSHQAPGEEKKLKCLAYDFYPGKIDVHWTFRAG--QVQEPPELRGDVNLHNGN 237
   | | | | : | | | : | : | : | : | : | : | : | : | : | : |
Db 180 QRADPPKTHVTHNPISDHEATLRCAWALGFYPAEITLTWQRDGEDQTDQTEI--VETRPAGD 238

QY 238 GTYOSWYVAVVPQDTAPYSCVHOSSLAQPLVVPWEAS 276
   | : | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 239 RTFOKMAAVVVPSSGEQRTYCHVQHEGLPKPLTLRWEPSS 277

```

Search completed: February 4, 2003, 10:06:01

Job time : 19 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 4, 2003, 10:03:00 : Search time 11 Seconds

(Without alignments)
1040.679 Million cell updates/sec

Title: US-09-701-463-1
Perfect score: 1504
Sequence: 1 QENQDGRYSLTFTYITGLSKH.....SCHVQHSLSLAQLVFPWEAS 276

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1487	98.9	295	1 ZA2G_HUMAN	P25311 homo sapien
2	901	59.9	296	1 ZA2G_RAT	O63678 rattus norv
3	877	58.3	307	1 ZA2G_MOUSE	O64726 mus musculu
4	527	35.0	362	1 IB02_HUMAN	P01889 homo sapien
5	524	34.8	362	1 IB39_HUMAN	P30460 homo sapien
6	519	34.5	362	1 IB19_HUMAN	Q08136 homo sapien
7	519	34.5	362	1 IB19_HUMAN	Q08136 gorilla gor
8	518	34.4	365	1 IOKO_GORGO	P30388 gorilla gor
9	517	34.4	338	1 IA01_PANTR	P16209 pan troglod
10	517	34.4	362	1 IB16_HUMAN	P30467 homo sapien
11	517	34.4	362	1 IB45_HUMAN	P30465 homo sapien
12	517	34.4	365	1 IB24_HUMAN	P05534 homo sapien
13	515	34.2	361	1 IB14_HUMAN	P03989 homo sapien
14	515	34.2	362	1 IB18_HUMAN	P10318 homo sapien
15	515	34.2	364	1 HA1B_BOVIN	P13753 bos taurus
16	514	34.2	362	1 IB59_HUMAN	P30496 homo sapien
17	513	34.1	365	1 IA23_HUMAN	P30447 homo sapien
18	512	34.0	354	1 IB24_HUMAN	P30470 homo sapien
19	512	34.0	362	1 IB22_HUMAN	P30468 homo sapien
20	511	34.0	362	1 IB15_HUMAN	P10317 homo sapien
21	511	34.0	362	1 IB32_HUMAN	P30476 homo sapien
22	510	33.9	362	1 IB27_HUMAN	P30492 homo sapien
23	510	33.9	362	1 IB55_HUMAN	P30492 homo sapien
24	510	33.9	362	1 IB57_HUMAN	P30494 homo sapien
25	509	33.8	362	1 IB04_HUMAN	P30460 homo sapien
26	509	33.8	359	1 IA11_HUMAN	P13746 homo sapien
27	508	33.8	362	1 IB01_PANTR	P16210 pan troglod
28	508	33.8	362	1 IA02_PANTR	P16210 pan troglod
29	508	33.8	362	1 IB02_PANTR	P13751 pan troglod
30	508	33.8	362	1 IB23_HUMAN	P30469 homo sapien
31	508	33.8	362	1 IB26_HUMAN	P30472 homo sapien
32	508	33.8	362	1 IB58_HUMAN	P30495 homo sapien
33	507	33.7	362	1 IB28_HUMAN	P30474 homo sapien

ALIGNMENTS

RESULT 1	2A2G_HUMAN	STANDARD:	PRT:	295 AA.
AC	P25311: 060386;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	zinc-alpha-2-glycoprotein precursor (zn-alpha-2-glycoprotein)			
DE	(zn-alpha-2-gp)			
GN	AZGP1 OR ZAG OR ZNGP1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate, and Liver;			
RX	MEDLINE=91264833; PubMed=2049092;			
RA	Ueyama H., Niwa M., Tada T., Sasaki M., Ohkubo I.;			
RT	"Cloning and nucleotide sequence of a human zn-alpha 2-glycoprotein			
RT	cDNA and chromosomal assignment of its gene.";			
RL	Biochem. Biophys. Res. Commun. 177:696-703(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RX	MEDLINE=92008677; PubMed=1915885;			
RA	Freije J.P., Fueyo A., Uribe J., Lopez-Otin C.;			
RT	"Human zn-alpha 2-glycoprotein cDNA cloning and expression analysis			
RT	in benign and malignant breast tissues.";			
RL	FEBS Lett. 290:247-249(1991).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94059971; PubMed=8241150;			
RA	Ueyama H., Deng H.X., Ohkubo I.;			
RT	"Molecular cloning and chromosomal assignment of the gene for human			
RT	zn-alpha 2-glycoprotein.";			
RL	Biochemistry 32:12968-12976(1993).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Leukocyte;			
RX	MEDLINE=94140356; PubMed=8307568;			
RA	Freije J.P., Fueyo A., Uribe J., Velasco G., Sanchez L.M.,			
RT	Lopez-Boado Y.S., Lopez-Otin C.;			
RT	"Human zn-alpha 2-glycoprotein: complete genomic sequence,			
RT	identification of a related pseudogene and relationship to class I			
RT	major histocompatibility complex genes.";			
RL	Genomics 18:575-587(1993).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Kalicki J., Harmon G.;			
RT	Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE OF 18-295.			
RC	TISSUE=Plasma;			
RX	MEDLINE=88124905; PubMed=3422450;			
RA	Araki T., Gejyo F., Takagaki K., Haupt H., Schwick H.G., Buerge W.,			

34	507	33.7	362	1 IB29_HUMAN	P18463 homo sapien
35	507	33.7	362	1 IB31_HUMAN	P30475 homo sapien
36	507	33.7	365	1 IA04_PANTR	P13749 pan troglod
37	507	33.7	366	1 IC02_GORGO	P30388 gorilla gor
38	507	33.7	366	1 IC04_GORGO	P30387 gorilla gor
39	506	33.6	362	1 IB34_HUMAN	O04826 homo sapien
40	505	33.6	365	1 IA03_PANTR	P13748 pan troglod
41	504	33.5	362	1 IB07_HUMAN	P30462 homo sapien
42	504	33.5	362	1 IB08_HUMAN	P30463 homo sapien
43	504	33.5	362	1 IB25_HUMAN	P30471 homo sapien
44	504	33.5	362	1 IB35_HUMAN	P30477 homo sapien
45	504	33.5	362	1 IB56_HUMAN	P30493 homo sapien

RA Marti T., Schaller J., Rickli E., Brossmer R., Atkinson P.H.,
RA Putnam F.W., Schmid K.;
RT "Complete amino acid sequence of human plasma Zn-alpha 2-glycoprotein
RT and its homology to histocompatibility antigens.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:679-683(1988).
RP CHARACTERIZATION, AND CRYSTALLIZATION.
RX MEDLINE=97272275; PubMed=9114041;
RA Sanchez L.M., Lopez-Otin C., Bjorkman P.J.;
RT "Biochemical characterization and crystallization of human Zn-alpha-2-
RT glycoprotein, a soluble class I major histocompatibility complex
RT homolog.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4626-4630(1997).
RP IN VITRO BINDING OF FATTY ACID.
RX MEDLINE=21433894; PubMed=11425849;
RA Kennedy M.W., Heikema A.P., Cooper A., Bjorkman P.J., Sanchez L.M.;
RT "Hydrophobic ligand binding by Zn-alpha 2-glycoprotein, a soluble
RT fat-depleting factor related to major histocompatibility complex
RT proteins.";
RL J. Biol. Chem. 276:35008-35013(2001).
RP [9]
RX X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RA MEDLINE=99217440; PubMed=10206894;
RA Sanchez L.M., Chirino A.J., Bjorkman P.J.;
RT "Crystal structure of human ZAG, a fat-depleting factor related to MHC
RT molecules.";
RL Science 283:1914-1919(1999).
CC -1- FUNCTION: Stimulates lipid degradation in adipocytes and causes
CC the extensive fat losses associated with some advanced cancers.
CC May bind polyunsaturated fatty acids.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Blood plasma, seminal plasma, urine, saliva,
CC sweat, epithelial cells of various human glands, liver.
CC -1- SIMILARITY: HIGH, TO THE EXTRACELLULAR DOMAIN OF THE ALPHA CHAIN
CC OF CLASS I MHC ANTIGENS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D90427; BAA14417.1; -;
DR EMBL: X59766; CAA42438.1; -;
DR EMBL: M76707; AAG61311.1; -;
DR EMBL: D14034; BAA03123.1; -;
DR EMBL: X69953; CAA49574.1; ALT_INIT.
DR EMBL: AC004522; AAC09483.1; -;
DR PIR: A31080; A31080.
DR PIR: J00946; J00946.
DR PDB: 1ZAG; 31-MAR-99.
DR SWISS-2DPAGE: P25311; HUMAN.
DR Genew: HGNC:910; AZGP1.
DR MIM: 194460; -;
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003597; Iq_C1.
DR InterPro: IPR001039; MHC_I.
DR Pfam: PF00047; 19; 2.
DR Pfam: PF00129; MHC_1; 2.
DR Prodom: PD000050; MHC_1; 1.
DR SMART: SM00407; IG1; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW Glycoprotein; Signal; 3D-structure.
FT CHAIN 1 17
FT MOD_RES 18 295 ZINC-ALPHA-2-GLYCOPROTEIN.
FT DISULFID 120 183 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 222 277
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .).
FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .).

FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .).
FT CONFLICT 1 2 MV -> MWASMSRL (IN REF. 2).
FT CONFLICT 82 82 O -> E (IN REF. 6).
FT CONFLICT 93 94 MISSING (IN REF. 6).
FT CONFLICT 241 241 E -> Q (IN REF. 6).
FT CONFLICT 266 295 AVPDPTAPYSGVHSSLAQPLVPMWEAS -> QCPRTQ
FT PTPATCSVAAPSPSCGPRARQGLAMDLRRSCPS
FT CLMEELNHRNHSQ ITHA (IN REF. 5).
SQ SEQUENCE 295 AA; 33872 MW; 6C6A7541A2B6371A CRC64;
Query Match 98.9%; Score 1487; DB 1; Length 295;
Best Local Similarity 98.6%; Pred. No. 1.5e-107;
Matches 274; Conservative 2; Mismatches 0; Indels 2; Gaps 1;
QY 1 QENDGRSLTYITYGTSKHEVDYPAQALGSLNDLFFRYNSDRKSOMGLMROVEGM 60
DB 18 QENDGRSLTYITYGTSKHEVDYPAQALGSLNDLFFRYNSDRKSOMGLMROVEGM 77
QY 61 EDKEDSOLAKARD--METLKDIVEYNDNSGSHVLOGRGCEIENNRSSGAEWXYVD 118
DB 78 EDWRDSDOLAKARDIMETLKDIVEYNDNSGSHVLOGRGCEIENNRSSGAEWXYVD 137
QY 119 GKDYIEFNKEIPAWVPDPDPAQITKQWEAPYVQRAKAYLEECATLTKYTKSKI 178
DB 138 GKDYIEFNKEIPAWVPDPDPAQITKQWEAPYVQRAKAYLEECATLTKYTKSKI 197
QY 179 LDRDPPSVVTSQAQGEKKKLCIADFPYGGKIDVHWTFAGVOPELRLGVLHNGG 238
DB 198 LDRDPPSVVTSQAQGEKKKLCIADFPYGGKIDVHWTFAGVOPELRLGVLHNGG 257
QY 239 TYQSWVVAVPPOPTAPYSCVHSHSLAQLVPMWEAS 276
DB 258 TYQSWVVAVPPOPTAPYSCVHSHSLAQLVPMWEAS 295
RESULT 2
ZAG_RAT ZAG_RAT STANDARD; PRT; 296 AA.
AC Q63678; Q63523;
ID 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DR 15-JUL-1999 (Rel. 38, Last annotation update)
DE Zinc-alpha-2-glycoprotein precursor (Zn-alpha-2-glycoprotein)
DE (Zn-alpha-2-GP).
CN AZGP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=95155283; PubMed=7852290;
RA Ueyama H., Naitoh H., Onkudo I.;
RT "Structure and expression of rat and mouse mRNAs for Zn-alpha 2-
RT glycoprotein.";
RL J. Biochem. 116:677-681(1994).
RN [2]
RP SEQUENCE OF 4-296 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=9433816; PubMed=8056339;
RA Fuenyo A., Uria J.A., Freije J.M.P., Lopez-Otin C.;
RT "Cloning and expression analysis of the cDNA encoding rat Zn-alpha 2-
RT glycoprotein.";
RL Gene 145:245-249(1994).
CC -1- FUNCTION: STIMULATES LIPID DEGRADATION IN ADIPOCYTES AND CAUSES
CC THE EXTENSIVE FAT LOSSES ASSOCIATED WITH SOME ADVANCED CANCERS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BUT NOT IN A WIDE NUMBER
CC OF TISSUES, INCLUDING PROSTATE, MAMMARY GLAND, KIDNEY, INTESTINE,
CC LUNG, PANCREAS, OVARY, UTERUS, THYROID, PLACENTA, SPLEEN, BRAIN
CC AND HEART.

```

CC -1- SIMILARITY: HIGH, TO THE EXTRACELLULAR DOMAIN OF THE ALPHA CHAIN
CC OF CLASS I MHC ANTIGENS.
CC -----
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CC -----
DR EMBL: D21058; BAA04637.1; -
DR EMBL: X75309; CAA53057.1; -
DR HSSP: P25311; 1ZAG.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR001039; MHC_I.
DR Pfam: PF00129; MHC_I; 1.
DR ProDom: PD000050; MHC_I; 1.
DR SMART: SM00410; Ig_Like; 1.
DR PROSITE: PS00290; IG_MHC; FALSE_NEG.
DR Glycoprotein; Signal.
KW SIGNAL
FT 1 17
FT CHAIN 18 296
FT MOD_RES 18 18
FT FT
FT FT
FT DISULFID 118 181
FT DISULFID 220 275
FT CARBOHYD 123 123
FT CARBOHYD 254 254
FT CONFLICT 120 120
FT CONFLICT 194 194
SQ SEQUENCE 296 AA; 34017 MW; 1259467DD18D4E3A CRC64;

Query Match 59.9%; Score 901; DB 1; Length 296;
Best Local Similarity 60.0%; Pred. No. 1,9e-62;
Matches 165; Conservative 39; Mismatches 65; Indels 6; Gaps 4;

QY 4 QDGRYSLTLYITGLSKHVEDVPAFOALGSLNDQFFRYNSKDRKSQPMGLMROVEGEMDW 63
DB 19 ETGSYSLTFLYTGLSRSKGLPRFOATAFLNDQAFHYNSNGSGAEVPMVSHVEGEMDW 78
QY 64 KEDSOLAKARED--METLKDIVEYNDNSGSHVLOGRFGCEIENNRSSGAFWKYYIDGKD 121
DB 79 EKESQLOARAREELFVLYLTKIMDYEDSTSGHTEFGMGCEITNNRSSGAVWRAYDGED 138
QY 122 YIEFNKEIPAWPDPDPAQAQITKQKWEAPYVORAKAYLEECPPATLRYLTKSKNLTDR 181
DB 139 FIEFNKEIPAWIPDPDPAANTKTKWEAEKYVORAKAYLEECPTMLKLYTSRSHLDR 198
QY 182 QDPPSVVVTSHOAPGEKKLKCLAYDFYPGKIDVHWTRAQ--VQPELGGDVLHNGNGT 239
DB 199 TDPPTVITSRVAPGRNRIRFRCIAYDFYPPORISLHMWQASKLAFEE-EG-VFPNGNGT 256
QY 240 YQSMVVAVVPPDPTAPYSCVHSHSLAQLPVPME 274
DB 257 YLSMVEVPPQNRDPFVCHIEHKLSQSLSYQMD 291

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=95155283; PubMed=7852290;
RA Ueyama H., Naitoh H., Ohkubo I.,
RT "Structure and expression of rat and mouse mRNAs for Zn-alpha 2-
RT glycoprotein.";
RL J. Biochem. 116:677-681(1994).
RN [2]
RP SEQUENCE OF 235-304 FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=95317827; PubMed=7797272;
RA Noguchi M., Kitabatake A., Ishihashi T., Kasahara M.;
RT "The MHC class I-like Zn-alpha 2-glycoprotein gene maps to mouse
RT chromosome 5.";
RL Immunogenetics 42:72-74(1995).
CC -1- FUNCTION: STIMULATES LIPID DEGRADATION IN ADIPOCYTES AND CAUSES
CC THE EXTENSIVE FAT LOSSES ASSOCIATED WITH SOME ADVANCED CANCERS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: HIGH, TO THE EXTRACELLULAR DOMAIN OF THE ALPHA CHAIN
CC OF CLASS I MHC ANTIGENS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D21059; BAA04638.1; -
DR EMBL: D44593; BAA07996.1; -
DR HSSP: P25311; 1ZAG.
DR MGD: MGI:103163; Azp1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR001039; MHC_I.
DR Pfam: PF00129; MHC_I; 1.
DR ProDom: PD000050; MHC_I; 1.
DR SMART: SM00410; Ig_Like; 1.
DR PROSITE: PS00290; IG_MHC; FALSE_NEG.
KW Glycoprotein; Signal.
FT 1 17
FT CHAIN 18 307
FT MOD_RES 18 18
FT FT
FT FT
FT DISULFID 118 181
FT DISULFID 220 275
FT CARBOHYD 123 123
FT CARBOHYD 190 190
FT CARBOHYD 254 254
SQ SEQUENCE 307 AA; 35256 MW; 4754524C76187A10 CRC64;

Query Match 58.3%; Score 877; DB 1; Length 307;
Best Local Similarity 59.3%; Pred. No. 1.4e-60;
Matches 163; Conservative 36; Mismatches 70; Indels 6; Gaps 4;

QY 4 QDGRYSLTLYITGLSKHVEDVPAFOALGSLNDQFFRYNSKDRKSQPMGLMROVEGEMDW 63
DB 19 ETGSYSLTFLYTGLSRSKGLPRFOATAFLNDQAFHYNSNGSGAEVPMVSHVEGEMDW 78
QY 64 KEDSOLAKARED--METLKDIVEYNDNSGSHVLOGRFGCEIENNRSSGAFWKYYIDGKD 121
DB 79 EKESQLOARAREELFVLYLTKIMDYEDSTSGHTEFGMGCEITNNRSSGAVWRAYDGED 138
QY 122 YIEFNKEIPAWPDPDPAQAQITKQKWEAPYVORAKAYLEECPPATLRYLTKSKNLTDR 181
DB 139 FIEFNKEIPAWIPDPDPAANTKTKWEAEKYVORAKAYLEECPPATLRYLTKSKNLTDR 198
QY 182 QDPPSVVVTSHOAPGEKKLKCLAYDFYPGKIDVHWTRAQ--VQPELGGDVLHNGNGT 239
DB 199 TDPPTVITSRVAPGRNRIRFRCIAYDFYPPORISLHMWQASKLAFEE-EG-VFPNGNGT 256

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RT Patham P lawlor D.A., Iomen C.E., Ennis P.D.: "The
RA "Diversity and diversification of HLA-A,B,C alleles.",
RL J. Immunol. 142:3937-3950(1989).
CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----
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CC -----
DR EMBL: M24034; AAA59667.1; -.
DR HSSP: P30460; IAGD.
DR MIM: 142830; -.
DR InterPro: IPRO03306; Ig_MHC.
DR InterPro: IPRO03597; Ig_c1.
DR InterPro: IPRO01039; MHC_I.
DR Pfam: PF00047; Ig_1.
DR Pfam: PF00129; MHC_I; 1.
DR PRODOM: PD000050; MHC_I; 1.
DR SMART: SM00407; IGc1; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT FT 25 362 BW*42 ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 299 309 CONNECTING PEPTIDE.
FT DOMAIN 310 333 CYTOPLASMIC TAIL.
FT DOMAIN 334 362 N-LINKED (GLCNAC. .) (BY SIMILARITY).
FT CARBOHD 110 110 BY SIMILARITY.
FT DISULFD 125 188 BY SIMILARITY.
FT DISULFD 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40333 MW; G9155AB015DA1BE CMC64;

Query Match 34.8%; Score 524; DB 1; Length 362;
Best Local Similarity 39.2%; Pred. No. 2.5e-33; Indels 10; Gaps 7;
Matches 111; Conservative 51; Mismatches 111;

OY 2 ENQGRYSLTITTYIGLSKSHVEDVPAFOALGSLNDFRRNS-KDKRSQPMGLRQVEG 59
DB 21 ETWACHSMKRFFYTSVSRRGPREFISGVYDDTFVRFSDAASPREEPARPIELEG 80
OY 60 MEDWKEDSLOLK-AREMETLKDIVEYYNDNS-GSHVLQGFCEI-ENNRSSGAFMKY 115
DB 81 PEYMWRNTQIKAKQOTRESLRNRGYNOSEASHLQSYGCDVPDGRLRGHNGY 140
OY 116 YTDGKOITFEKNKEIPAWVPDPAAQITOKKAEPEVVORAKAYIEECPPATLRKYLS 175
DB 141 AYDGKDYIALNEDLSRWTAADTAQAITORKWEAARV-AEOBRAYLEGTCEWLRYRENG 199
OY 176 KNILDRQRPSPVNVYSHAAPGEKKLKLCLAVDFYCKIDIVMTFRAG--QVQEPRLRGVL 233
DB 200 KDTLERAPRPTHVHHHSIDHEATLRKWAIGFYAEITLLTWQRGDEDOTDTEL-VETR 258
OY 234 HNGNGTYOSVVVAVPPODTAPYSCHVQGHSSIAQLPVLPMEAS 276
DB 259 PAGDRTPFKMAAVVYPVSGEQRYTCVQHGEGLPKLTIRWPS 301

RESULT 6
ID 1B19_HUMAN STANDARD; PRT; 362 AA.
AC 008136;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
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DE DT 16-OCT-2001 (Rel. 40, last annotation update)
DE HLA class I histocompatibility antigen, B-27 B*2706 alpha chain
DE precursor.
GN HLA-B OR HLAB.
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94102824; PubMed=8276469;
RA Vilches C., de Pablo R., Kreisler M.;
RT "Nucleotide sequence of HLA-B*2706.";
RL Immunogenetics 39:219-219(1994) .
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96134006; PubMed=8550101;
RA Ruckaleit M., Bowness P., Wordsworth P.;
RT "The nucleotide sequence of HLA-B*2704 reveals a new amino acid
RT substitution in exon 4 which is also present in HLA-B*2706.";
RL Immunogenetics 43:160-162(1996) .
CC CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) .
CC CC -----
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CC or send an email to license@isb-sib.ch) .
CC CC -----
DR EMBL: X73578; AAC51980.1; -
DR EMBL: U035734; AAC50447.1; -
DR DR HSSP: P03989; HBSA.
DR DR MIM: 142830; -
DR DR InterPro: IPR003006; IG_MHC.
DR DR InterPro: IPR003597; IG_CL.
DR DR InterPro: IPR001039; MHC_I.
DR DR Pfam: PF00047; Ig; 1.
DR DR Pfam: PF00129; MHC_I; 1.
DR DR Pfam: PD000050; MHC_I; 1.
DR DR SMART: SM00407; IGc1; 1.
DR DR PROSITE: PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
KY FT SIGNAL
FT 1 24
FT CHAIN 25 362
FT FT
FT FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT FT B-27 B*2706 ALPHA CHAIN.
FT FT DOMAIN 25 114
FT FT DOMAIN 115 206
FT FT DOMAIN 207 298
FT FT DOMAIN 299 308
FT FT DOMAIN 309 332
FT FT TRANSMEM 333 362
FT FT CARBOHYD 110 110
FT FT DISULFID 125 188
FT FT DISULFID 227 283
FT FT CONFLICT 235 235
FT FT SEQUENCE 362 AA; 40456 MW; B5F5CE95000C487 CRC64;
SO
Query Match 34.5%; Score 519; DB 1; Length 362;
Best Local Similarity 38.5%; Pred. No. 5,9e-33;
Matches 109; Conservative 50; Mismatches 114; Indels 10; Gaps
QY 2 ENQDGRSLTYLYTGLSKHVEDPAFQALGSLNDLQFFRYSN-KDRKSQPMGLMROYEG 59
DB 21 ETWAGSHSMRFHTSVSPRGCEPRFITVGYVDTLFVRPDSADASPREEPRAPWIDEG 80
QY 60 MEDWKEQSOL-QKAREDEMTKLQIVLEYNDNS-GSHVLOGRFQCELT-ENNRSSAFPMKY 115
DB 81 PEYWDREFOICKAKQOTRESLRTLLRRLYNDSEASGSHLQNMWYGCDAVPDRDLRLNGDYQY 140

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Qy	116	YVDDKQVTEENFKELIPAWPPEDPAQOIKRQKEAEVYVQRAKALTEECSPATLRRKYLS	175
Db	141	AYDKEDYALIEDLSSWAAADPAQIITQKWEAAR-EAEQI-RATIEGSCVMILRYLENG	199
Qy	176	KNILDRDDPPPVVVTYSHQAPQEKRLKCLADFPYGGKIDVHMTAG--QVQPELIRGDLV	233
Db	200	KETIGRADPRPTHTVTHHPSIDHEATLRGMALGEPVAETITLMWRGDEQOTDEL-VETR	258
Qy	234	HNGCTQSWVVAVVAPPODTAPYGSCHVQSHSLAOPLYVPMAS	276
Db	259	PAGRTFQKMAVVVPSGEORVTCVQHEDLPRLTLMWPS	301
RESULT 7			
ID	10KO.GORGO	STANDARD;	PRT; 362 AA.
AC	P30388;		
DT	01-APR-1993 (Rel. 25, Created)		
DT	01-APR-1993 (Rel. 25, Last sequence update)		
DT	01-APR-1993 (Rel. 25, Last annotation update)		
DS	Class 1 histocompatibility antigen, GOGO-OKO alpha chain precursor.		
OS	Gorilla gorilla gorilla (Lowland gorilla).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Gorilla.		
OX	NCBI_TaxID=9595;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
R3	MEDLINE=92078860; PubMed=1744581;		
RA	Lawlor D.A., Warren E., Taylor P., Parham P.;		
RT	"Gorilla class I major histocompatibility complex alleles: comparison		
RT	to human and chimpanzee class I."		
RL	J. Exp. Med. 174:1491-1509(1991).		
CC	-1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO		
CC	THE IMMUNE SYSTEM.		
CC	-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-		
CC	MICROGLOBULIN).		
CC	-----		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; X60692; CAA43100.1; -		
DR	PIR; JH0538; JH0538.		
DR	HSSP; P30685; IABE.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003597; IG_C1.		
DR	InterPro; IPR001039; MHC_I.		
DR	Pfam; PF00047; Ig_1.		
DR	Pfam; PF00129; MHC_I_1.		
DR	ProDom; PD000050; MHC_I_1.		
DR	SMART; SM00407; IGC1_1.		
DR	PROSITE; PS00290; IG_MHC_1.		
KW	MHC I; Transmembrane; Glycoprotein; Signal.		
FT	SIGNAL	1	24
FT	CHAIN	25	362
FT			
FT	DOMAIN	25	114
FT			
FT	DOMAIN	115	206
FT			
FT	DOMAIN	207	298
FT			
FT	DOMAIN	299	308
FT			
FT	TRANSMEM	309	332
FT			
FT	DOMAIN	333	362
FT			
FT	DISULFID	125	188
FT			
FT	DISULFID	227	283
FT			
FT	CAROHND	110	110
FT			
SO	SEQUENCE	362 AA;	40755 MW;
Query Match 34.5%; Score 519; DB 1; Length 362;			

[illegible]

ID	1A01_PANTR	STANDARD:	PRT:	365 AA.
AC	P16209;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	01-APR-1993 (Rel. 25, Last annotation update)			
DE	CH1A class I histocompatibility antigen, A-2 alpha chain precursor.			
OS	Pan troglodytes (Chimpanzee).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.			
OX	NCBI_Taxid=9598;			
RN	[1]			
RE	SEQUENCE FROM N.A.			
RX	MEDLINE=90201944; PubMed=1690682;			
RA	Lawlor D.A., Warren E., Ward F.E., Parham P.;			
RT	"Comparison of class I MHC alleles in humans and apes.";			
RL	Immunol. Rev. 113:147-185(1990).			
CC	-1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO			
CC	THE IMMUNE SYSTEM.			
CC	-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-			
CC	MICROGLOBULIN).			
CC	-----			
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CC	-----			
DR	EMBL; M30678; AAA87970.1; -			
DR	HSSE; Q95352; 1HKH.			
DR	InterPro: IPR003006; IG_MHC.			
DR	InterPro: IPR003597; IG_C1.			
DR	InterPro: IPR001039; MHC_I.			
DR	Pfam: PF00047; Ig; 1.			
DR	Pfam: PF00129; MHC_I; 1.			
DR	ProDom: PD000050; MHC_I; 1.			
DR	SMART; SM00407; IGc1; 1.			
DR	PROSITE; PS00290; IG_MHC; 1.			
KW	MHC I; Transmembrane; Glycoprotein; Signal.			
FT	SIGNAL	1	24	
FT	CHAIN	25	365	
FT				CH1A CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT				A-2 ALPHA CHAIN.
FT	DOMAIN	25	114	EXTRACELLULAR ALPHA-1.
FT	DOMAIN	115	206	EXTRACELLULAR ALPHA-2.
FT	DOMAIN	207	298	EXTRACELLULAR ALPHA-3.
FT	DOMAIN	299	308	CONNECTING PEPTIDE.

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FT TRANSMEM 309 332 CYTOPLASMIC TAIL.
FT DOMAIN 333 365 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
SQ SEQUENCE 365 AA; 4084 MW; FC452786BD038D3E CRC64;

Query Match 34.4%; Score 518; DB 1; Length 365;
Best Local Similarity 40.0%; Pred. No. 7.2e-33;
Matches 114; Conservative 46; Mismatches 103; Indels 22; Gaps 9;

QY 6 GRYSLTYITGLSKHVEDPAPFQALGSLNDLOFPYNS--KDRKSQPMGLMROYEGMEDW 63
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 25 GSHSMRYFTSVSRGCEPRFTVGYDDTLFVRFSDAASPREPAPMIEDGPEYW 84
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 64 KEDSOLA-----REDMETLKDIVEYNDN--GSHVLOGRFCEIENNRSGAFMKRYK 116
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 85 DEETSAFAHSQTDVDTLGLRG--YYNQSDDGSHTIQIMYCDV--GSDGRFLRGYR 138
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 117 --YDGKDYIEFNKEIPAPVPEPDAQITKQWEAEPYVORAKAYLEECPATLRYLYK 173
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 139 QDAYGKRYIALNEDLRMTADMAAOITKRMEAHAAEQR--RAYLEGTCYEMLRILE 197
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 174 YSKNILDROPSSVVTSHQAPGEEKKLKCLAYDFPGKIDVHWTFRAG--QVQPELREGD 231
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 198 NGKETLQRTDPRKTHHTHPISDHEATLRCAWALGFYPAEITLTMQRDGEDQTDTEL-VE 256
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 232 VLNHNGNGYGSWVAVVPQDTAPYSCHVHSSLAOPLVVPEAS 276
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 257 TRPADGTGFKMAAVVPSGEGRYTCHVHGELPKPLTLRMERS 301
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 9
1B20_HUMAN STANDARD; PRT; 338 AA.
ID 1B20_HUMAN STANDARD; PRT; 338 AA.
AC P30467;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, B*27 B*2707 alpha chain
   (B*27-HS).
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CX Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
GX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91268545; PubMed=1711072;
RA Choo Y.S., Pan L.A., Hansen J.A.;
RT "A novel HLA-B*27 allele maps B27 allotypespecificity to the region around
   position 70 in the alpha 1 domain."
RL J. Immunol. 147:174-180(1991).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
   THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
   MICROGLOBULIN).
CC -----
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DR Pfam; PF00129; MHC_I; 1.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGL; 1.
DR PROSITE; PS00290; IGL_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein.
FT DOMAIN 1 90 EXTRACELLULAR ALPHA-1.
FT DOMAIN 91 182 EXTRACELLULAR ALPHA-2.
FT DOMAIN 183 274 EXTRACELLULAR ALPHA-3.
FT DOMAIN 275 284 CONNECTING PEPTIDE.
FT TRANSMEM 285 308
FT DOMAIN 309 338 CYTOPLASMIC TAIL.
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT DISULFID 101 164 BY SIMILARITY.
FT DISULFID 203 259 BY SIMILARITY.
SQ SEQUENCE 338 AA; 37804 MW; B6529066c87317c7 CRC64;

Query Match 34.4%; Score 517; DB 1; Length 338;
Best Local Similarity 39.1%; Pred. No. 7.8e-33;
Matches 109; Conservative 48; Mismatches 112; Indels 10; Gaps 7;

QY 6 GRYSLTYITGLSKHVEDPAPFQALGSLNDLOFPYNS--KDRKSQPMGLMROYEGMEDW 63
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1 GSHSMRYFTSVSRGCEPRFTVGYDDTLFVRFSDAASPREPAPMIEDGPEYW 60
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 64 KEDSOL--QKAREDEMETLKDIVEYNDN--GSHVLOGRFCEI--ENNRSGAFMKRYK 119
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 61 DREITQKAKAQTDRDRLTLRYNQSAGSHLQSMYCGDVGPDRLHGHNGYAYDG 120
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 120 KDYLEFNKEIPAWVPEPDAQITKQWEAEPYVORAKAYLEECPATLRYLYKSKIL 179
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 121 KDYIALNEDLRMTADMAAOITQKWEAARV--AEOLRAYLEGCEVLEMLRYLENGKETL 179
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 180 DROPPSSVVTSHQAPGEEKKLKCLAYDFPGKIDVHWTFRAG--QVQPELREGDVLHNGN 237
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 180 QADPPKTHVTHHPISDHEATLRCAWALGFYPAEITLTMQRDGEDQTDTEL-VETRPAGD 238
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 238 GYGSWVAVVPQDTAPYSCHVHSSLAOPLVVPEAS 276
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 239 RTFKMAAVVPSGEGRYTCHVHGELPKPLTLRMERS 277
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 10
1B16_HUMAN STANDARD; PRT; 362 AA.
ID 1B16_HUMAN STANDARD; PRT; 362 AA.
AC P19373;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, B*27 B*2703 alpha chain
   precursor (B-27p).
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CX Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
GX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88227491; PubMed=3286582;
RA Choo Y.S., St John T., Orr H.T., Hansen J.A.;
RT "Molecular analysis of the variant allotype HLA-B*27d (HLA-B*2703)
   identifies a unique single amino acid substitution."
RL Hum. Immunol. 21:209-219(1988).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
   THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
   MICROGLOBULIN).
CC -----
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   or send an email to license@isb-sib.ch).
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or send an email to license@lsb-sib.ch).

CC EMBL; M54883; AAA59616.1; .
DR HSSP; P03989; IHS.
DR MIM; 142830; .
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IgC1; 1.
DR PROSITE; PS00290; Ig_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 115 206 B-27 B*2703 ALPHA CHAIN.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-1.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 309 332 EXTRACELLULAR ALPHA-3.
FT DOMAIN 333 362 CONNECTING PEPTIDE.
FT DOMAIN 110 110 CYTOPLASMIC TAIL.
FT CARBOHYD 125 188 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT DISULFID 227 283 BY SIMILARITY.
FT SEQUENCE 362 AA; 40402 MW; 8CC7B45FE899036 CRC64;
SQ

Query Match 34.4%; Score 517; DB 1; Length 362;
Best Local Similarity 38.5%; Pred. No. 8.5e-33;
Matches 109; Conservative 49; Mismatches 115; Indels 10; Gaps 7;

QY 2 ENODGRYSLTITYTGLSKHVEDVPAFQALGSLNDQFFRYNS-KDRKSQPMGLMROYEG 59
DB 21 ETWAGSHSMRYHTSRSRGEPRTITGYDDTLFVFDSDATSPKREPAPIEDBG 80
QY 60 MEDWKEDSOL-QKAREMETLKDIVEYYNDSN-GSHVLOGRFGCEI-ENNSSGAFMKY 115
DB 81 PEYMBRETOISKNTQYREDRTL-LRYYNQSEAGSHTLQRMFGCDVGPDRILRGY 140
QY 116 YDGDQDYIEFNKEIPAWVPDPDPAQITTKQWEAPYVORAKAYLEEECPATLRKYLKS 175
DB 141 AYDGKDYIALNEDLSWTADTAADTAQITTKQWEAPYVORAKAYLEEECPATLRKYL 199
QY 176 KNLIDRQDPSPVYVTSQAPGEGKKLCLAYDFYCKIDVHMTBAG-OVQPEELRG 233
DB 200 KETIQADRPKPKVHTHPISDHEATLRCAWALGYFAETILTLQROGDEDTOTDEL-VETR 258
QY 234 HNGNGTYGSMVYVAVPDPDPAQITTKQWEAPYVORAKAYLEEECPATLRKYL 276
DB 259 PAGDRTRFKMAVAVVPSGGEORVYTCVHOGELPKPLTLMEPS 301

RESULT 11
ID 1B45_HUMAN STANDARD: PRT; 362 AA.
AC P30485;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, BW-47 B*4701 alpha chain precursor.
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=8152906; PubMed=3257938;
RA Zemmour J., Enlis P.D., Parham P., Dupont B.;
RT "Comparison of the structure of HLA-Bw47 to HLA-B13 and its relationship to 21-hydroxylase deficiency.";

Immunogenetics 27:281-287(1988).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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CC EMBL; M19756; AAA52664.1; .
DR HSSP; P03989; IHS.
DR MIM; 142830; .
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IgC1; 1.
DR PROSITE; PS00290; Ig_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 115 206 B-47 B*4701 ALPHA CHAIN.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-1.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 309 332 EXTRACELLULAR ALPHA-3.
FT DOMAIN 333 362 CONNECTING PEPTIDE.
FT DOMAIN 110 110 CYTOPLASMIC TAIL.
FT CARBOHYD 125 188 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT DISULFID 227 283 BY SIMILARITY.
FT SEQUENCE 362 AA; 40571 MW; EDD3EACB8C15EAE CRC64;
SQ

Query Match 34.4%; Score 517; DB 1; Length 362;
Best Local Similarity 39.2%; Pred. No. 8.5e-33;
Matches 112; Conservative 45; Mismatches 113; Indels 16; Gaps 8;

QY 2 ENODGRYSLTITYTGLSKHVEDVPAFQALGSLNDQFFRYNS-KDRKSQPMGLMROYEG 59
DB 21 ETWAGSHSMRYHTSRSRGEPRTITGYDDTLFVFDSDATSPKREPAPIEDBG 80
QY 60 MEDWKEDSOLQKAREMETLKDIVEYYNDSN-GSHVLOGRFGCEI-ENNSSGAF 112
DB 81 PEYMBRETOISKNTQYREDRTL-LRYYNQSEAGSHTLQRMFGCDVGPDRILRGY 137
QY 113 WKYYDGKDYIEFNKEIPAWVPDPDPAQITTKQWEAPYVORAKAYLEEECPATLRKYL 172
DB 138 HODAYDGKDYIALNEDLSWTADTAADTAQITTKQWEAPYVORAKAYLEEECPATLRKYL 196
QY 173 KYSKNLIDRQDPSPVYVTSQAPGEGKKLCLAYDFYCKIDVHMTBAG-OVQPEELRG 230
DB 197 ENGKETIQADRPKPKVHTHPISDHEATLRCAWALGYFAETILTLQROGDEDTOTDEL-V 255
QY 231 DYLHNGNGTYGSMVYVAVPDPDPAQITTKQWEAPYVORAKAYLEEECPATLRKYL 276
DB 256 ETRPAGDRTRFKMAVAVVPSGGEORVYTCVHOGELPKPLTLMEPS 301

RESULT 12
ID 1A24_HUMAN STANDARD: PRT; 365 AA.
AC P05534; P30448; P30449; Q95355;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, A-24(A-9) alpha chain

DE precursor (A*24).
GN HLA-A OR HLA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A. (A*2401).
RX MEDLINE=85206128; PubMed=287115;
RA Nguyen C., Sodoyer R., Trucy J., Strachan T., Jordan B.R.;
RT "the HLA-A*24 gene: sequence, surroundings and comparison with the
HLA-A2 and HLA-A3 genes";
RL Immunogenetics 21:479-489(1985).
RN [2]
RN REVISIONS (A*2401).
RA Jordan B.R.;
RL Submitted (XXX-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A. (A*2402/A*2403).
RX MEDLINE=92104637; PubMed=1729171;
RA Little A.-M., Madrigal J.A., Parham P.;
RT "Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3";
RL Immunogenetics 35:41-45(1992).
RN [4]
RN SEQUENCE FROM N.A. (A*2402).
RX MEDLINE=92269955; PubMed=1317015;
RA Belich M.P., Madrigal J.A., Hildebrand W.H., Zemmour J.,
RA Williams R.C., Luz R., Petzl-Erler M.L., Parham P.;
RT "Unusual HLA-B alleles in two tribes of Brazilian Indians";
RL Nature 357:326-329(1992).
RN [5]
RN SEQUENCE FROM N.A. (A*2402).
RX MEDLINE=98007772; PubMed=9349616;
RA Laforet M., Froelich N., Parisiadis A., Bausinger H., Pfeiffer B.,
RA Tongio M.M.;
RT "An intronic mutation responsible for a low level of expression of an
HLA-A*24 allele";
RL Tissue Antigens 50:340-346(1997).
RN [6]
RN SEQUENCE OF 26-206 FROM N.A.
RA Gao X., McCluskey J.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [7]
RN SEQUENCE FROM N.A. (A*2408).
RA Tissue-Blood;
RA Kishikawa K., Tokunaga K., Ishikawa Y., Qiu L., Furuya M.,
RA Sawanaka K., Akaza T., Tadokoro K., Uji T.;
RT "A new A9 sequence HLA-A9HH from Japanese";
RL MHC 3:9-14(1996).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
CC -1- POLYMORPHISM: THE FOLLOWING ALLELES OF A-24 ARE KNOWN: A*2401,
A*2401, A*2403 AND A*2408 (A9HH). THE SEQUENCE SHOWN IS THAT OF
A*2401.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M15497; AAA59611.1; -;
DR EMBL: M64740; AAA59601.1; -;
DR EMBL: M64741; AAA59601.1; -;
DR EMBL: U19733; AAB60651.1; -;
DR EMBL: U19887; AAB60651.1; JOINED.
DR EMBL: Z72422; CAA96532.1; -;
DR EMBL: D83516; BAA11936.1; -;
DR HSSP: Q95352; IHKK.

DR MM: 142800; -;
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR001039; MHC_I.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00129; MHC_I; 1.
DR ProDom: PD000050; MHC_I; 1.
DR SMART: SM00407; IGcl; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 24
FT CHAIN 25 365
FT
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 365
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT VARIANT 5 5
FT
FT VARIANT 27 27
FT
FT VARIANT 86 86
FT
FT VARIANT 89 89
FT
FT VARIANT 180 180
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FT VARIANT 190 191
FT
FT VARIANT 206 206
FT
SQ SEQUENCE 365 AA; 40644 MW; 7BDD98AADEFEAE3 CRC64;
Query Match 34.4%; Score 517; DB 1; Length 365;
Best Local Similarity 39.8%; Pred. No. 8.6e-33;
Matches 111; Conservative 46; Mismatches 112; Indels 10; Gaps 7;
QY 6 GYSLTYYTGLSKHVEDVPAFOALGSLNDQFFRYNS-KDRKSOPGLMROYEGMEDW 63
DB 25 GSHSKRIFSTSVSRGRREPRFIAVGYDDTQYFARFSDASQMRPAPRIBDGPETW 84
QY 64 KESQLOKA-REDMETLKDIVEYYNDNS-GSHVLOGRFGCEI-ENNRSGAFMKYYVDG 119
DB 85 DEITGVKVAHSQTDRENRLRLRYNQSAGSHLQWFMFGDVGSDGFLRGYHQYAVDG 144
QY 120 KDYLEFNKEIPAWVPDPDAOITKOKFEAPYVYORAKAYLEECPTALKYLYKNIL 179
DB 145 KDYLALKEDRLSWTAADMAAOITKRKWEAAHV-AEOQAYLEYGTCVGLRYYLNGKETT 203
QY 180 DRDPPSVVYVTSQAPRGKRLKCLAVDFYPGKIDVHMTFRAG-OYOEPELRGDLVNGN 237
DB 204 QRADPKTHMTHHPISDHEATRLRCWALGFYPAETLTLNQRGEDOTDTTEL-VETRPAGD 262
QY 238 GYSQWVVAVPDPTAPYSCVOHSSLAQPLVVPWEMS 276
DB 263 GTFQKMAVVVPSGEGRYTCVQVHGSLPKPLTLRWERS 301
RESULT 13
ID 1B14 HUMAN STANDARD; PRT; 361 AA.
AC P03989;
DT 23-OCT-1986 (Rel. 02, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, B-27 alpha chain precursor.
GN HLA-B OR HLA-B.

OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. PubMed=3912316;
 RA MEDLINE=86138405; Lang M., Riethmuller G.,
 RA Weiss E.H., Kuon W., Doerner C.,
 RT "Organization, sequence and expression of the HLA-B*27 gene: a
 RT molecular approach to analyze HLA and disease associations";
 RL Immunobiology 170:367-380(1985).
 RN [2]
 RP SEQUENCE OF 25-361 FROM N.A.
 RA MEDLINE=86149317; PubMed=3485286;
 RA Szeles H., Riethmuller G., Weiss E., Meo T.,
 RT "Complete sequence of HLA-B*27 CDNA identified through the
 RT characterization of structural markers unique to the HLA-A, -B, and
 RT -C allelic series";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986).
 RN [3]
 RP SEQUENCE OF 25-295.
 RA MEDLINE=85226361; PubMed=2408663;
 RA Ezquerro A., Bragado R., Vega M.A., Strominger J.L., Woody J.,
 RT Lopez de Castro J.A.;
 RT "Primary structure of papain-solubilized human histocompatibility
 RT antigen HLA-B*27";
 RL Biochemistry 24:1733-1741(1985).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 25-300.
 RA MEDLINE=92405152; PubMed=1525820;
 RA Madden D.R., Gorga J.C., Strominger J.L., Wiley D.C.;
 RT "The three-dimensional structure of HLA-B*27 at 2.1 Å resolution
 RT suggests a general mechanism for tight peptide binding to MHC";
 RL Cell 70:1035-1048(1992).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY.
 RA MEDLINE=92018187; PubMed=1922337;
 RA Madden D.R., Gorga J.C., Strominger J.L., Wiley D.C.;
 RT "The structure of HLA-B*27 reveals a nonamer self-peptides bound in an
 RT extended conformation";
 RL Nature 353:321-325(1991).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC -1- DISEASE: THIS PROTEIN CORRELATES WITH THE DEVELOPMENT OF
 CC ANKYLOSING SPONDYLITIS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, X03945; CAA27578.1; ALT_TERM.
 DR PIR: S07441; S07441.
 DR PDB: 1HSA; 15-OCT-92.
 DR MIM: 142830;
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_C1.
 DR InterPro: IPR001039; MHC_I.
 DR Pfam: PF00047; Ig_1.
 DR Pfam: PF00129; MHC_I_1.
 DR ProDom: PD000050; MHC_I_1.
 DR SMART: SM00407; IgC1_1.
 DR PROSITE: PS00290; Ig_MHC; 1.
 KW MHC_I: Transmembrane; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 361 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-27 ALPHA CHAIN.

FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 308
 FT TRANSMEM 309 332
 FT DOMAIN 333 361
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT CONFLICT 206 206
 FT CONFLICT 266 266
 FT STRAND 27 38
 FT TURN 39 41
 FT STRAND 42 52
 FT TURN 53 54
 FT STRAND 55 61
 FT TURN 62 63
 FT STRAND 70 71
 FT HELIX 74 76
 FT TURN 77 78
 FT HELIX 81 108
 FT TURN 109 110
 FT TURN 113 114
 FT STRAND 118 127
 FT TURN 129 130
 FT STRAND 133 142
 FT TURN 143 144
 FT STRAND 145 150
 FT TURN 152 153
 FT STRAND 157 159
 FT HELIX 162 173
 FT TURN 174 175
 FT HELIX 176 185
 FT HELIX 186 186
 FT HELIX 187 198
 FT TURN 199 199
 FT HELIX 200 203
 FT TURN 204 204
 FT STRAND 207 207
 FT STRAND 210 217
 FT STRAND 222 233
 FT STRAND 238 243
 FT TURN 244 245
 FT STRAND 246 247
 FT HELIX 249 251
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 FT STRAND 258 259
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 FT TURN 275 276
 FT HELIX 281 286
 FT STRAND 288 289
 FT STRAND 294 296
 SQ SEQUENCE 361 AA; 40464 MW; 2F8293299B52A47F CRC64;
 Query Match 34.2%; Score 515; DB 1; Length 361;
 Best Local Similarity 38.5%; Pred. No. 1.2e-32;
 Matches 109; Conservative 49; Mismatches 115; Indels 10; Gaps 7;
 QY 2 ENODGRYSLTLYTGTGSKHEDVDPFAQALGSLNDLFERYNS--KDRKSQPMGLRQVEG 59
 DB 21 ETWAGSHSMRYFHTSVSRGRGEPRFTYGVYDPLFVAFDSDASPREPRAPMIEDCG 80
 QY 60 MEDWKEEDSQL--OKAREDEMTLKDIVEYYNDSN--GSHVLQGRFGCEI--ENNSSCAFMYK 115
 DB 81 PEYWDRETIQKAKAQOTDREDLRTILRYYNQSEAGSHTLQNNYGCQDVGPDGRLRGYHOD 140
 QY 116 YTDGADYIEFNKEIPAWVFPDPAQITKQKWAEPYVYQRAAYLEEDCPATLRKYIKS 175
 DB 141 AYDGKXYIALNDELISWTADTAQAQITQRKKWAARY--AEQLRAYLEGCEVWLRRYLENG 199
 QY 176 KNILRODDEPSVYVYVSHQAPGKKKLCCLAYDYFGKIDVHMTTRAG--QVQPEPLRGDVL 233

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Db      200 KETTLORAPPKTVHHHPISIDHEATLRCWALGFEYPAEITLLTQNRGDGEQTOTTEL-VEHR 258
Oy      234 HNGNCTQSVMVAVNPDPDTAFYSCHVOHSSLAQFLVVPMWEAS 276
          | : | : | | | : | : | | | | | | : | : | | |
Db      259 PAGDRTFQRMAVAVPVSSEGRRYTCHVQHGLPKEPLTRMPEPS 301
RESULT 14
ID      IB18_HUMAN STANDARD; PRT; 362 AA.
AC      PI0318;
DT      01-MAR-1989 (Rel. 10, Created)
DT      01-MAR-1989 (Rel. 10, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      HLA class I histocompatibility antigen, B-27*B*2705 alpha chain
DE      precursor (B-*27w) (B27.1).
OS      HLA-B OR HLAB.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX      NCBI_taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=86220133; PubMed=3011111;
RA      Seemann G.H.A., Rein R.S., Brown C.S., Ploegh H.L.;
RT      "Gene conversion-like mechanisms may generate polymorphism in human
RT      class I genes.";
RL      EMBO J. 5:547-552(1986).
[2]
RN      [3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=86138405; PubMed=3912316;
RA      Weiss E.H., Kuon W., Doerner C., Lang M., Riethmuelier G.;
RT      "Organization, sequence and expression of the HLA-B27 gene: a
RT      molecular approach to analyze HLA and disease associations.";
RL      Immunobiology 170:367-380(1985).
[3]
RN      [3]
RP      3D-STRUCTURE MODELING OF 11S-206.
RX      MEDLINE=95148615; PubMed=7846047;
RA      Rognan D., Scapozza L., Folkers G., Daser A.;
RT      "Rational design of nonnatural peptides as high-affinity ligands for
RT      the HLA-B*2705 human leukocyte antigen";
RL      Proc. Natl. Acad. Sci. U.S.A. 92:753-757(1995).
-I      FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
         THE IMMUNE SYSTEM.
CC      -I SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
         MICROGLOBULIN).
-----
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-----
DR      EMBL; X03665; CAAG27302.1; .
DR      EMBL; X03666; CAA27302.1; JOINED.
DR      EMBL; M12667; AAA36221.1; -.
DR      PIR; A25092; HLHNBW
DR      PDB; 1ROG; 30-SEP-94.
DR      PDB; 1ROH; 30-SEP-94.
DR      PDB; 1ROI; 30-SEP-94.
DR      PDB; 1ROJ; 30-SEP-94.
DR      PDB; 1ROL; 30-SEP-94.
DR      PDB; 1ROK; 30-SEP-94.
DR      PDB; 1ROU; 30-SEP-94.
DR      MIR; 142830; .
DR      InterPro; IPRO03006; Ig_MHC.
DR      InterPro; IPRO03597; Ig_cl.
DR      InterPro; IPRO01039; MHC_I.
DR      Pfam; PF00047; Ig; 1.
DR      Pfam; PF00129; MHC_I; 1.
DR      ProDom; PD000050; MHC_I; 1.
DR      SMART; SMO0407; IGCL; 1.
```

```

DR PROSITE: PS00290; IG-MHC: 1.
KM MHC I; Transmembrane; Glycoprotein; Signal; 3d-structure.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 B-27 B*2705 ALPHA CHAIN.
FT FT 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 N-LINKED GLYCANC. . . ) (BY SIMILARITY).
FT DISULFD 125 188 BY SIMILARITY.
FT DISULFD 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40428 MW; C8D2F154E3292031 CRC64;

Query Match 34.2%; Score 515; DB 1; Length 362;
Best Local Similarity 38.5%; Pred. NO. 1.2e-32;
Matches 109; Conservative 49; Mismatches 115; Indels 10; Gaps 7;

OY 2 ENODRYSLTITYTYGTSLKHVEDVPAFOALGSLNDLOFFRYS--KDRKSQPMGLMROVEG 59
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 21 EFWASHSHSRMYHTSVSRGREGREFRFTYGYVDLTLFRFSDASPRREPAPYIEDEG 80
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

OY 60 MEDWEDSOL--OKAREDMETLKDIVEEYNDNS-GSHVLCGREGCI-ENNSSGAFMKY 115
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 81 PEYMWREFOICAKAQOTREDRLTLRLRYNOSEAGSHFLONNYGCDVGDGPDGLLRYGHQD 140
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

OY 116 YVDCGDYIEFNKEFIAWVPFDPAAITQOKWAEVYVYQAKAYLEECSPATLRKYLKYS 175
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 141 AVDGKDYIALNEDLSSWPAADTAADTAQITQKRWAAAV-AEQLNAVYLEGECVEMLRYLENG 199
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

OY 176 KNLILROPSPVAVYVSHOAPGEEKKILKCLAYFEGKIDVHMTFRAG--QVQEPFLRGDVL 233
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 200 KETLGRADPEKTHVYHNPISDHEALTRCMALGFYAEILITLMQRRGEQDTQDTFL-VEFR 258
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

OY 234 HNGNGTYGSWVAVVPQDTAPYSCHVOHSSLAQPLVVPWEAS 276
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 259 PAGDRTFOKMAVVVPVSGEEGRYTCVQHGLPKPLTLRMEPS 301
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 15
HAIB_BOVIN STANDARD; PRT; 364 AA.
ID HAIB_BOVIN
AC P13753;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-JAN-1990 (Rel. 13, Last annotation update)
DE BOLA class I histocompatibility antigen, alpha chain BL3-7 precursor.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88258075; PubMed=3133413;
RA Enlis P.D., Jackson A.P., Parham P.;
RT "Molecular cloning of bovine class I MHC cDNA.";
RL J. Immunol. 141:642-651(1988).
CC 1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----
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OM protein - protein search, using sw model

Run on: February 4, 2003, 10:03:20 ; Search time 33 Seconds

(without alignments)
1723.303 Million cell updates/sec

Title: US-09-701-463-1

Perfect score: 1504
Sequence: 1 QENQDGRYSLTYITGLSKH.....SCHVQHSLSLAQPLVPMWAS 276

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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SPTREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	871	57.9	307	11	Q9DBB7
2	527	35.0	336	7	019782
3	527	35.0	362	7	029854
4	527	35.0	362	7	031613
5	526	35.0	362	7	09P95
6	526	35.0	362	7	P79489
7	523	34.8	356	7	030221
8	523	34.8	362	7	Q9MXK1
9	523	34.8	362	7	Q29681
10	523	34.8	362	7	Q9MXK4
11	522	34.7	357	7	030894
12	522	34.7	362	7	029638
13	522	34.7	362	7	029861
14	521	34.6	355	7	Q9MXJ8
15	521	34.6	355	7	095529
16	520	34.6	357	7	Q30895

17	520	34.6	362	7	Q9MXL9
18	520	34.6	362	7	Q9TPW6
19	520	34.6	362	7	Q9MXI0
20	520	34.6	362	7	P79612
21	520	34.6	362	7	Q29846
22	520	34.6	362	7	Q29718
23	519	34.5	354	7	Q95412
24	519	34.5	354	7	078204
25	519	34.5	362	7	Q29705
26	519	34.5	362	7	P79555
27	518	34.4	354	7	Q95525
28	518	34.4	362	7	Q29689
29	517	34.4	298	7	Q9GJF1
30	517	34.4	362	7	Q9GIL3
31	517	34.4	362	7	Q29693
32	517	34.4	365	7	Q95J06
33	516	34.3	354	7	Q95527
34	516	34.3	362	7	Q9MXH0
35	516	34.3	362	7	Q9MYB8
36	516	34.3	362	7	Q30720
37	516	34.3	365	7	Q9XRX7
38	515	34.2	360	7	Q95396
39	515	34.2	362	7	Q78189
40	515	34.2	365	7	Q9MY51
41	514	34.2	346	7	Q30897
42	514	34.2	357	7	Q9MXJ3
43	514	34.2	359	7	Q29934
44	514	34.2	362	7	Q9MXH5
45	514	34.2	365	7	Q8WLNO

ALIGNMENTS

```

RESULT 1
ID Q9DBB7 PRELIMINARY; PRT; 307 AA.
AC Q9DBB7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE Alpha-2-glycoprotein 1, zinc.
GN AGPl.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LIVER;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki K., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carinetti P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki K., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK005051; BAB23777.1; -.
HSSP; P25311; 1ZAG.

```


Oy	2	ENOGRSILTYITGSKHVEDPAFOALGSLUNDLOFFPNYS--KDRKSOPMLTROVEG	59
		1: : : : : 1: : : : : 1: : : : : 1: : : : :	
Db	21	ETWAGSHSMRFYTSVRPGRGEPRTISVGYVDDTQFVFRSDSASPREEPAPIEDGB	80
		1: : : : : 1: : : : : 1: : : : : 1: : : : :	
Oy	60	MEDMKEDSOLQ--AREDMETLADIVEYYDNS--GSHVLQGRGCEI--ENNSSGAFWKY	115
		1: : : : : 1: : : : : 1: : : : : 1: : : : :	
Db	81	PEYDMRMTQTKAAQODRSLNLRNGYUNOSGASHTQSGMCGVPGDGLTNGHOY	140
		1: : : : : 1: : : : : 1: : : : : 1: : : : :	
Oy	116	YUDDKDYIEFNKEITPAWPPDPAAOITTKOMEPEPVYORAKAYLEECBPATLRKLYKS	175
		1: : : : : 1: : : : : 1: : : : : 1: : : : :	
Db	141	AYDGDIDYALNEDLRSTADTAAQITQKMEAKAREABOR--RYVLEGCEVEMLRITLENG	199
		1: : : : : 1: : : : : 1: : : : : 1: : : : :	
Oy	176	KNILRODPPBSVVVTSQAOBGEKKIKLCLAIYDEPGKIDVHMTFRAG--OVQPELIRGDVL	233
		1: : : : : 1: : : : : 1: : : : : 1: : : : :	
Db	200	KDKLERADPPRTHTVHNPIDSHDEATLRCLMGLGEPYPAETITLQORGDODTOTEL--VEIR	258
		1: : : : : 1: : : : : 1: : : : : 1: : : : :	
Oy	234	HNGNGTOSMYYVAVPQDPAPYSCYHOHSLAOPILVYMEAS	276
		1: : : : : 1: : : : : 1: : : : : 1: : : : :	
Db	259	PAGDRTFOKMAVVPBGGEORITCYHQHEGLKPKPLTLEWBS	301
		1: : : : : 1: : : : : 1: : : : : 1: : : : :	

RESULT 4
Q31613
ID Q31613
PRELIMINARY;
PRT; 362 AA.

DT	01-NOV-1996	(TREMBLrel. 01, Created)
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)
DT	01-JUN-2002	(TREMBLrel. 21, last annotation update)
DE	MHC class I antigen heavy chain precursor.	
GN	HLA-B.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_Taxid=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=96128250; PubMed=8537119;	
RA	Smith K.D., Epperson D.F., Lutz C.T.;	
RT	"Alloreactive cytotoxic T-lymphocyte-defined HLA-B7 subtypes differ in	
RT	peptide antigen presentation."	
RL	Immunogenetics 43:27-37(1996).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=95184211; PubMed=7878658;	
RA	Arnett K.L., Adams E.J., Domena J.D., Parham P.;	
RT	"Structure of a novel subtype of B7 (B*0705) isolated from a Chinese	
RT	individual."	
RL	Tissue Antigens 44:318-321(1996).	
CC	-1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE	
CC	IMMUNE SYSTEM (BY SIMILARITY).	
CC	-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-	
CC	MICROGLOBULIN) (BY SIMILARITY).	
DR	EMBL: U21052; AAA92563.1; -;	
DR	EMBL: L33922; AAA65639.1; -;	
DR	HSSP; P30460; IAGD.	
DR	InterPro: IPR003597; Ig_c1.	
DR	InterPro: IPR003006; Ig_MHC.	
DR	InterPro: IPR001039; MHC_1.	
DR	Pfam: PF00047; Ig_1.	
DR	Pfam: PF00129; MHC_1; 1.	
DR	PRINTS; PR01638; MHCCLASSI.	
DR	ProDom; PD000050; MHC_1; 1.	
DR	SMART; SM00407; Ig_c1; 1.	
DR	PROSITE; PS00290; IG_MHC_1.	
KW	Glycoprotein; MHC; Signal; Transmembrane.	
FT	SIGNAL	1 24
FT	CHAIN	25 362
FT	SEQUENCE	362 AA; 4047 MW; CDFB36D9FFCDD5A CRC64;
		MHC CLASS I ANTIGEN HEAVY CHAIN.

Query Match	35.0%;	Score 527;	DB 7;	Length 362;
Best Local Similarity	39.9%;	Pred. No. 1.9e-37;		
Matches 113;	Conservative 49;	Mismatches 111;	Indels 10;	Gaps 77;

[illegible]

RESULT 5
Q9TP95
ID Q9TP95 PRELIMINARY; PRT; 362 AA.

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DT 01-MAY-2000 (TREMBLrel. 13, Created)
DR 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE MHC class I antigen.
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bettinotti M.P., Hadzikadic L., Dhillon G., Barracchini K.,
RA Martincola F.M.;
RT "A new HLA-B allele.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
EMBL AF189017: AAF01052.1; -.
DR HSSP: P30460; IAGD.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003506; Ig_MHC.
DR InterPro: IPR01039; MHC_I.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00129; MHC_I; 1.
DR PRINTS: PRO1638; MHCCLASSI.
DR PRODOM: PD000050; MHC_I; 1.
DR SMART: SM00407; IGc1; 1.
DR PROSITE: PS00290; IG_MHC; 1.
DR Glycoprotein; Transmembrane.
KW SEQUENCE 362 AA; 40541 MW; 92A0ACC3DCDC2747 CRC64;

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Query Match	35.0%;	Score 526;	DB 7;	Length 362;
Best Local Similarity	39.6%;	Pred. No. 2.4e-37;		
Matches 112;	Conservative 51;	Mismatches 110;	Indels 10;	Gaps 7

QY 2 ENOGRSLATITVYLKSHVEDVAFALCSLNDJOFFRRNS--KDKRSOPMGLMRVCG 59
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 21 ETMAGSHSMRFRYTSVPBGCEPRFTISVGVDOTGVRFDSOAASPREBRAPWIDEG 80

QY 60 MEDKKESOLOK--ARDMEFLKDIVERYSNDS-GSHVLORGCET-ENNSSGAFWKY 115
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 81 PEYMDRNQTILKAQAQDRESLRNLTNGTYMSSEAGSHITDRMGDCDGPGRLLRGHDYT 140

QY 116 YDGKDYIEENKEIPAWVPEDPAAQITKOWEAEPPYVRQAKAVLEECPATLRKTKYLS 175
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
141 AYSDKDKIALUNEDIRSTMADTAQAOTIQRKWEAAREAEOR-RAYLEECVCJEWLRRLYLENG 199

QY 176 KNILRODPPSVVYTSQAAPGEEKKLCLAYDFPGKIDVHMTFRAG--QVQEPRLRGDVL 233
ID 030221 PRELIMINARY; PRT; 362 AA.
AC P79489;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE HLA-B*52.2.
GN HLA-B*5504.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homalidae; Homo.
NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLLOOD;
RA Bannai M., Tokunaga K., Tanaka H., Kashiwase K., Lin L., Tokunaga K.,
Jui T.;
RT "Five HLA-B*22 group alleles in Japanese."
RL Tissue Antigens 0:0-0(1997).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN) (BY SIMILARITY).
DR EMBL: D85761; BAA12868.1; -.
DR HSSP; P30460; IAGD.
DR InterPro; IPR003597; Iq_c1.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Iq; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IqC1; 1.
DR PROSITE; PS00290; Iq_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 362 AA; 40484 MW; 2FEE2B98C0B5F5BF CRC64;

Query Match 35.0%; Score 526; DB 7; Length 362;
Best Local Similarity 39.6%; Pred. No. 2,4e-37;
Matches 112; Conservative 48; Mismatches 113; Indels 10; Gaps 7;
QY 2 ENQDGRYSITLYITGTSKHEVDVPAFQALGSLNDQFFRYNS--KDRKSQPMGLRQVEG 59
ID 030221 PRELIMINARY; PRT; 362 AA.
AC P79489;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE HLA-B*52.2.
GN HLA-B*5504.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homalidae; Homo.
NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLLOOD;
RA Bannai M., Tokunaga K., Tanaka H., Kashiwase K., Lin L., Tokunaga K.,
Jui T.;
RT "Five HLA-B*22 group alleles in Japanese."
RL Tissue Antigens 0:0-0(1997).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN) (BY SIMILARITY).
DR EMBL: D85761; BAA12868.1; -.
DR HSSP; P30460; IAGD.
DR InterPro; IPR003597; Iq_c1.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Iq; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IqC1; 1.
DR PROSITE; PS00290; Iq_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 362 AA; 40484 MW; 2FEE2B98C0B5F5BF CRC64;

QY 21 EFWASHSKRYITLTAMSRGSEPRFIAGVDDTQFVFFDSDAISPREPRAPMEQSG 80
ID 030221 PRELIMINARY; PRT; 362 AA.
AC P79489;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE HLA-B*52.2.
GN HLA-B*5504.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homalidae; Homo.
NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLLOOD;
RA Bannai M., Tokunaga K., Tanaka H., Kashiwase K., Lin L., Tokunaga K.,
Jui T.;
RT "Five HLA-B*22 group alleles in Japanese."
RL Tissue Antigens 0:0-0(1997).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN) (BY SIMILARITY).
DR EMBL: D85761; BAA12868.1; -.
DR HSSP; P30460; IAGD.
DR InterPro; IPR003597; Iq_c1.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Iq; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IqC1; 1.
DR PROSITE; PS00290; Iq_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 362 AA; 40484 MW; 2FEE2B98C0B5F5BF CRC64;

RESULT 7
QY 176 KNILRODPPSVVYTSQAAPGEEKKLCLAYDFPGKIDVHMTFRAG--QVQEPRLRGDVL 233
ID 030221 PRELIMINARY; PRT; 362 AA.
AC P79489;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE HLA-B*52.2.
GN HLA-B*5504.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homalidae; Homo.
NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLLOOD;
RA Bannai M., Tokunaga K., Tanaka H., Kashiwase K., Lin L., Tokunaga K.,
Jui T.;
RT "Five HLA-B*22 group alleles in Japanese."
RL Tissue Antigens 0:0-0(1997).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN) (BY SIMILARITY).
DR EMBL: D85761; BAA12868.1; -.
DR HSSP; P30460; IAGD.
DR InterPro; IPR003597; Iq_c1.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Iq; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IqC1; 1.
DR PROSITE; PS00290; Iq_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 362 AA; 40484 MW; 2FEE2B98C0B5F5BF CRC64;

Query Match 34.8%; Score 523; DB 7; Length 362;
Best Local Similarity 39.1%; Pred. No. 4,2e-37;
Matches 113; Conservative 50; Mismatches 104; Indels 22; Gaps 9;
QY 2 ENQDGRYSITLYITGTSKHEVDVPAFQALGSLNDQFFRYNSKDR--KSQPMGLRQVEG 59
ID 030221 PRELIMINARY; PRT; 362 AA.
AC P79489;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE HLA-B*52.2.
GN HLA-B*5504.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homalidae; Homo.
NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLLOOD;
RA Bannai M., Tokunaga K., Tanaka H., Kashiwase K., Lin L., Tokunaga K.,
Jui T.;
RT "Five HLA-B*22 group alleles in Japanese."
RL Tissue Antigens 0:0-0(1997).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN) (BY SIMILARITY).
DR EMBL: D85761; BAA12868.1; -.
DR HSSP; P30460; IAGD.
DR InterPro; IPR003597; Iq_c1.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Iq; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IqC1; 1.
DR PROSITE; PS00290; Iq_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 362 AA; 40484 MW; 2FEE2B98C0B5F5BF CRC64;

QY 60 MEDKEDSLOKA-----REDMETKLDIYEVYNSN--GSHVLOGRFGCEI--ENNSSGAFW 113
ID 030221 PRELIMINARY; PRT; 362 AA.
AC P79489;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE HLA-B*52.2.
GN HLA-B*5504.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homalidae; Homo.
NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLLOOD;
RA Bannai M., Tokunaga K., Tanaka H., Kashiwase K., Lin L., Tokunaga K.,
Jui T.;
RT "Five HLA-B*22 group alleles in Japanese."
RL Tissue Antigens 0:0-0(1997).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN) (BY SIMILARITY).
DR EMBL: D85761; BAA12868.1; -.
DR HSSP; P30460; IAGD.
DR InterPro; IPR003597; Iq_c1.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Iq; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IqC1; 1.
DR PROSITE; PS00290; Iq_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 362 AA; 40484 MW; 2FEE2B98C0B5F5BF CRC64;

QY 114 KYK----YDKDYIEFNKEIPAWPEFPAQAQITKQKWEAPYVORAKAYLEECPPATLR 169
ID 030221 PRELIMINARY; PRT; 362 AA.
AC P79489;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE HLA-B*52.2.
GN HLA-B*5504.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homalidae; Homo.
NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLLOOD;
RA Bannai M., Tokunaga K., Tanaka H., Kashiwase K., Lin L., Tokunaga K.,
Jui T.;
RT "Five HLA-B*22 group alleles in Japanese."
RL Tissue Antigens 0:0-0(1997).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN) (BY SIMILARITY).
DR EMBL: D85761; BAA12868.1; -.
DR HSSP; P30460; IAGD.
DR InterPro; IPR003597; Iq_c1.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Iq; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IqC1; 1.
DR PROSITE; PS00290; Iq_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 362 AA; 40484 MW; 2FEE2B98C0B5F5BF CRC64;

GN PATR-B.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
OX NCBI_TaxId=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=20322475; PubMed=10866106;
RA de Groot N.G., Oting N., Arguello R., Watkins D.I., Doxiadis G.G.M.,
Madrizal J.A., Bontrop R.E.,
RT "Major histocompatibility complex class I diversity in a West African
Chimpanzee population: implications for HIV research.";
RL Immunogenetics 51:398-409(2000).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; AF168410; AAF72791.1; -.
DR HSSP; P03989; ILSA.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR01039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PRO1638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; Igcl; 1.
DR PROSITE; PS00290; Ig_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 362 AA; 40442 MW; 4E1A081945D3A4F3 CRC64;

Query Match 34.8%; Score 523; DB 7; Length 362;
Best local similarity 39.6%; Pred. No. 4.3e-37;
Matches 112; Conservative 46; Mismatches 115; Indels 10; Gaps 7;

QY 2 ENODGRSLTYITVGLSKHVEDVPAFOALGSLNDLOEFRRYSKDR--KSQPMGLMROVEG 59
Db 21 ETWAGSGSMRYFTYMSRGRGEPRIYGVYDQFVRFSDDAIPMEGRPAWIEDEG 80
QY 60 MEDKEDSQ--LQKAREMELTKDIVERYYNDN-GSHVLQGRFGCEI-ENNRSSGAFWKY 115
Db 81 PEYDNRNTQITKTQADRENILRTLLRYNOSSEAGSHTLQSGMDGDPDRLLRGHDY 140
QY 116 YDDGKDYIEFKETIPAWPFPDPAQITQKWEAEPPVYVQRAKAYLEECPTLTKRYLYKS 175
Db 141 AYDGDYIALNKDDSSWADTAQITQKWEAARV-AEQLRAYLEGTCVEMLRYLENG 199
QY 176 KNILRDPPSVVVTSHQAPGEKKKLCIAYDFYPGKIDVHMTAG--QVOEPELRGDVL 233
Db 200 KETIQRADPRKTHVTHHPSIDEHATLRGMALGFYPAETITLWQDGEQDQDTEL-VETR 258
QY 234 HNGKTYOSWVVAVPPDPTAPYCHVOHSSLAQPLVVPWEAS 276
Db 259 PAGDRTFQKMAAVVVPSSGEQRYTCHVQHEGLPKPLTLRWEPS 301
RESULT 9
Q29681 PRELIMINARY; PRT; 362 AA.
ID Q29681
AC Q29681;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE MHC class I antigen heavy chain precursor.
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96128250; PubMed=8537119;

RA Smith K.D., Epperson D.F., Lutz C.T.;
RT "Alloreactive cytotoxic T-lymphocyte-defined HLA-B7 subtypes differ in
peptide antigen presentation.";
RL Immunogenetics 43:27-37(1996).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; U21053; AAA92564.1; -.
DR HSSP; P30460; IAGD.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR01039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PRO1638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; Igcl; 1.
DR PROSITE; PS00290; Ig_MHC; 1.
KW Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 24
FT CHAIN 25 362 MHC CLASS I ANTIGEN HEAVY CHAIN.
SQ SEQUENCE 362 AA; 40506 MW; 563D142F5507BC98 CRC64;

Query Match 34.8%; Score 523; DB 7; Length 362;
Best local similarity 39.6%; Pred. No. 4.3e-37;
Matches 112; Conservative 49; Mismatches 112; Indels 10; Gaps 7;

QY 2 ENODGRSLTYITVGLSKHVEDVPAFOALGSLNDLOEFRRYS--KDRKSQPMGLMROVEG 59
Db 21 ETWAGSHSMRYFTYSRGRGEPRIYGVYDQFVRFSDDAASPREBRPAWIEDEG 80
QY 60 MEDKEDSLOK--AREMELTKDIVERYYNDN-GSHVLQGRFGCEI-ENNRSSGAFWKY 115
Db 81 PEYDNRNTQITKTQADRENILRTLLRYNOSSEAGSHTLQSGMDGDPDRLLRGHDY 140
QY 116 YDDGKDYIEFKETIPAWPFPDPAQITQKWEAEPPVYVQRAKAYLEECPTLTKRYLYKS 175
Db 141 AYDGDYIALNKDDSSWADTAQITQKWEARENR-RAYLEGTCVEMLRYLENG 199
QY 176 KNILRDPPSVVVTSHQAPGEKKKLCIAYDFYPGKIDVHMTAG--QVOEPELRGDVL 233
Db 200 KDKLERADPRKTHVTHHPSIDEHATLRGMALGFYPAETITLWQDGEQDQDTEL-VETR 258
QY 234 HNGKTYOSWVVAVPPDPTAPYCHVOHSSLAQPLVVPWEAS 276
Db 259 PAGDRTFQKMAAVVVPSSGEQRYTCHVQHEGLPKPLTLRWEPS 301
RESULT 10
Q9MKK4 PRELIMINARY; PRT; 362 AA.
ID Q9MKK4
AC Q9MKK4;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE MHC class I antigen (lymphocyte antigen).
GN PATR-B OR PATR-B17.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
OX NCBI_TaxId=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=20322475; PubMed=10866106;
RA de Groot N.G., Oting N., Arguello R., Watkins D.I., Doxiadis G.G.M.,
Madrizal J.A., Bontrop R.E.,
RT "Major histocompatibility complex class I diversity in a West African
Chimpanzee population: implications for HIV research.";
RL Immunogenetics 51:398-409(2000).
RN [2]
RP SEQUENCE FROM N.A.


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DR ProdDom: PD000050; MHC_I: 1.
DR SMART: SM00407; ICc1: 1.
DR PROSITE: PS00290; IG_MHC: 1.
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	Query Match	Similarity	Best Local	Matches	Conservative	Score 521	DB 7	Length 355
2	ENODRYSLTYYTYSLSKSHVEDVPAFOALGSLINDIOFRYNS--KDRKSOPGMLRWQEG	34.6%	38.9%	110	48	115	10	Gaps 7

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Db      13  ETWASHSHSRKRYTTSVSRGRGEPRTITGVYDDTQFVAFEDDAASPRAEPAPMEDEG 72
QY      60  MEDMKEDSOLQK--AREDETLDIYEYNDNSN-GSHVLQGRFGEI-ENNSSGAFMWY 115
Db      73  PEYWDRETRNMKASQTDRENRLRIALRYNQSSEASHIIRKRYGDMGDLGLNGYQY 132
QY      116 YDGDYIEFNKEIPAWVPDPAAQITKQKWEAEVYVORAKAYLEECBPATLRKYLKYS 175
Db      133 AYDGKDYIALNEDLSSWTAAADTAQAQITQKWEAARAQR-RAYLEGTCEVWLRRLYLENG 191
QY      176 KNIIDRDPSPVYVTSQAPEKKKLCIAYFPYFKIDVHWTFRAG--QVQPELRGDVL 233
Db      192 KETLGRADPPKTHVTHHPISDHEATLRCAWALGFYPAETITLTMQRDGEDQTDTEL-VETR 250
QY      234 HNGNGTYOSWYVAVVPDDTAPYSCHVQSSLAQPLVVPMEAS 276
Db      251 PEGDRTFQKMAVAVVPSGEEQRYTCHVQHEGLPKPLTLRMEPS 293

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RESULT 15

095529

ID 095529 PRELIMINARY; PRT: 355 AA.

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AC 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
EF 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Class I histocompatibility antigen (Fragment).
GN HLA-B.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_Taxid=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TEPRFE.
RX MEDLINE=94286544; PubMed=8016085;
RA McAdam S.N., Boyson J.E., Liu X., Garber T.L., Hughes A.L.,
RA Bontrop R.E., Watkins D.I.;
RT "A uniquely high level of recombination at the HLA-B locus.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:5893-5897(1994).
CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
CC EMBL: U05580; AAA50183.1; -.
DR HSSP: P03989; IHSa.
DR InterPro: IPR003597; Ig_CL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR01039; MHC_I.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00129; MHC_I; 1.
DR PRINTS: PR01638; MHCCLASSI.
DR PRODOM: PD000050; MHC_I; 1.
DR SMART: SM00407; IgCL; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
FT NON_TER
SQ SEQUENCE 355 AA; 39772 MW; F474A2C3EEDC398A CRC64;

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Query Match 34.6%; Score 521; DB 7; Length 355;

Best Local Similarity 38.9%; Pred. No. 6, 2e-37; Matches 110; Conservative 48; Mismatches 115; Indels 10; Gaps 7;

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QY      2  ENDGGRYSLTYYITGLSKHVEDPAPQALGSLNDLQFFRYS--KDRKSQPMGLMROVGS 59
Db      13  ETWAGSHSMRYTTSVSRGRGEPRTITGVYDDTQFVRPDSAPSRMEPRAPWLEQEG 72
QY      60  MEDMKEDSOLQK--AREDETLDIYEYNDNSN-GSHVLQGRFGEI-ENNSSGAFMWY 115
Db      73  PEYWDRETRNMKASQTDRENRLRIALRYNQSSEASHIIRKRYGDMGDLGLNGYQY 132
QY      116 YDGDYIEFNKEIPAWVPDPAAQITKQKWEAEVYVORAKAYLEECBPATLRKYLKYS 175

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Db      133 AYDGKDYIALNEDLSSWTAAADTAQAQITQKWEAARAQR-RAYLEGTCEVWLRRLYLENG 191
QY      176 KNIIDRDPSPVYVTSQAPEKKKLCIAYFPYFKIDVHWTFRAG--QVQPELRGDVL 233
Db      192 KETLGRADPPKTHVTHHPISDHEATLRCAWALGFYPAETITLTMQRDGEDQTDTEL-VETR 250
QY      234 HNGNGTYOSWYVAVVPDDTAPYSCHVQSSLAQPLVVPMEAS 276
Db      251 PEGDRTFQKMAVAVVPSGEEQRYTCHVQHEGLPKPLTLRMEPS 293

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Search completed: February 4, 2003, 10:05:37
Job time : 35 secs